

STIC-Biotech/ChemLib

179876 Search notes

From: Chan, Christina
Sent: Friday, February 17, 2006 9:09 AM
To: Sitton, Jehanne Souaya; STIC-Biotech/ChemLib
Subject: RE: rush search for an after final

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
FEB 17 2006
(STIC)

-----Original Message-----

From: Sitton, Jehanne Souaya
Sent: Friday, February 17, 2006 8:05 AM
To: Chan, Christina
Subject: rush search for an after final

Christina,
Please forward this rush request to STIC. It's for an afterfinal.

Please perform an interference search for the following: 1) nucleotides 1-1407 of
SEQ ID NO: 1 and 2) nucleotides 11200-12800 for SEQ ID NO: 1 in application
09/673,476.

↳ this is a mistake - Stic
searched 1533 base pairs

thanks,
Jehanne Sitton
Primary Examiner
Art Unit 1634
Rem-2D81 (office)
Rem-2C70 (mailbox)
571-272-0752

from position 11199-
12732
of Seq 1

Searcher: Noble
Searcher Phone: _____
Date Searcher Picked up: 2/17/06
Date completed: 2/21/06
Searcher Prep Time: 5
Online Time: 5

Type of Search
NA# 2 AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: compugen
WWW/Internet: _____
Other (Specify): _____

11

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QY 301 TTGTGTCACATGCTCAGGCTCGACAGCGCGCTCGAGCCGGAGGCGCCACACATCCACGA 360
Db 11500 TTGTGTCACATGCTCAGGCTCGACAGCGCGCTCGAGCCGGAGGCGCCACACATCCACGA 11559
QY 361 GCCCCTCGGGCTCGGCTCGGCGCGGAGCTTGGCCACTCGGCTCTTGAAGCCGCGCG 420
Db 11560 GCCCCTCGGGCTCGGCTCGGCGCGGAGCTTGGCCACTCGGCTCTTGAAGCCGCGCG 11619
QY 421 CGGGTGTGCCCGCGGCTCGAGCGCCAGCATGCGAGTCCGCGGATGCGCGCGGATGG 480
Db 11620 CGGGTGTGCCCGCGGCTCGAGCGCCAGCATGCGAGTCCGCGGATGCGCGCGGATGG 11679
QY 481 TTTCCTGACGCGCGCGCCCTCGGCGCTCGGAACGTTGCGATCTCGCGCAAGATCC 540
Db 11680 TTTCCTGACGCGCGCGCCCTCGGCGCTCGGAACGTTGCGATCTCGCGCAAGATCC 11739
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QY 721 ACATGCGGATGTCGCATCACCGGTGCGGACGTGCGATACAGTCCAGGGGATCA 780
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QY 781 CGTGCGCAGGAATGCTGTAGCGCTCGAGCGACGCTTACCGCGCGGATGTTGTCGGA 840
Db 11980 CGTGCGCAGGAATGCTGTAGCGCTCGAGCGACGCTTACCGCGCGGATGTTGTCGGA 12039
QY 841 TCAAGTTCAATCAAGATCAACGATCAGGCTCAAGTTGCCCGCGCACCCCGAGGCGGA 900
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Db 12100 ACTTCAGTCTTGGATGCGCGTCTCCCATATCACTCGGACGGGATGGAAGCACACCG 12159
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Db 12160 TCGTCTTGGGGTGC CGGTTCAGGAATGCGACTGTTGCTTACGCGATCGATCC 12219
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Db 12220 AGTAGTCTCGCGCTCGCACAGCGGACGTACTCGCGCGAGGGCGGACAGGGCGCGG 12279
QY 1081 TCAGGTTCCATTGAGCGCGAGGTTTTCGTCTCGAAGATCGCCGGAAACAGTTCGGGT 1140
Db 12280 TCAGGTTCCATTGAGCGCGAGGTTTTCGTCTCGAAGATCGCCGGAAACAGTTCGGGT 12339
QY 1141 ACCGCTCGGCGTACTCACGGATGATCGCGGGGTGSCATCGGTTCGACGCTCGTCGGGCA 1200
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QY 1201 CGATGATCTCACCGGGAAAGTGGTTGTGCTCGAGAAAGCTGTGCAAGGCTTCACCGG 1260
Db 12400 CGATGATCTCACCGGGAAAGTGGTTGTGCTCGAGAAAGCTGTGCAAGGCTTCACCGG 12459
QY 1261 CGTAGCCCGCTGTTGTGAGTGTGCGACCATGCTCACTTGGGGCAAAAGCTGGGAC 1320
Db 12460 CGTAGCCCGCTGTTGTGAGTGTGCGACCATGCTCACTTGGGGCAAAAGCTGGGAC 12519
QY 1321 TCACGCTCGGCGCTTTTCTCGCGCGCCCGCAAGGGTATTGCGATGCGCAACGTGAATCGC 1380
Db 12520 TCACGCTCGGCGCTTTTCTCGCGCGCCCGCAAGGGTATTGCGATGCGCAACGTGAATCGC 12579
QY 1381 CTGTGCGCGCGCGCTGCGCGCTGTTGCGCTGTTGCTGCGCGGAGCTACGGCACACGCT 1440

Db 12580 CTGTGCGCGCGCGCTGCGCGCTGTTGCTGTTGCTGCGCGGAGCTACGGCACACGCT 12639
QY 1441 GCCGAAGTATACCGAGGGTGCACCTGACGTTGGGCTCGAAACCGCGTGGCGCGGTTGGG 1500
Db 12640 GCCGAAGTATACCGAGGGTGCACCTGACGTTGGGCTCGAAACCGCGTGGCGCGGTTGGG 12699
QY 1501 CCACCGCTTCAGATCGGTGCTGGTTGGCTCGC 1533
Db 12700 CCACCGCTTCAGATCGGTGCTGGTTGGCTCGC 12732

RESULT 2
US-09-670-314-1
; Sequence 1, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-1

Query Match 100.0%; Score 1533; DB 3; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTCAGCTCCGGAACCTCGATCCCGAGGACCTGAAATCCCATCGCGCGCAACCCGACC 60
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QY 61 GGTACCCGCTTCCAAGCAGCGACATCGCGCAGCGTAGGTGGCTCTTGTCCCGGGA 120
Db 11260 GGTACCCGCTTCCAAGCAGCGACATCGCGCAGCGTAGGTGGCTCTTGTCCCGGGA 11319
QY 121 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGCTTAACGTGGC 180
Db 11320 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGCTTAACGTGGC 11379
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 240
Db 11380 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 11439
QY 241 ACCGCGCGCGCGCAATGTTCTGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 300
Db 11440 ACCGCGCGCGCGCAATGTTCTGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 11499
QY 301 TTTGTGCAATGGTCAAGCTCGACAGCGCGTCCGAGCGCGGAGGCGCAACATCCACGA 360
Db 11500 TTTGTGCAATGGTCAAGCTCGACAGCGCGTCCGAGCGCGGAGGCGCAACATCCACGA 11559
QY 361 GCCCCTCGGCTCGGCGTCCGCGGAGCTTCGCCACCTCGGCTTGGGCTTTGAGCCCGCG 420
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QY 721 ACATGCGCATGTGCGCATCAGCGGTGCGGACGTGACAGTACACAGTCCAGGGGCATGA 780
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QY 781 CGTCGCGCAGGAATGTCTGTAGCGCTCGAGCGCGACGGTACACGGCCGAGTTGGTCTGGA 840
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QY 841 TGAAGTTTCATCAAGATCAACGATCAGAGCTCAAGTTGCCCGCGCACCCCGAACCAGGGGGGA 900
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QY 901 ACTTCGAGTCTTGGCATCGCGCTCTCCATATCACTCGGACGGGATGGAAGCACACCG 960
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Db 1708303 TCGTCTTGGGGTGC CGGTGCGAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1708362
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Db 1708663 TCACCGTCTGCGCCCTTTTCTGCGCGCGCGCAAGGGTATTGCGATGGCGAACGTGAATCGC 1708722
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QY 1441 GCGGAAGTATAGCAGGGTGCATGACGTTGGCTCGAAACCGCGTGGCGCGGCTGTGGG 1500
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QY 1501 CGCACCGTCTCGAGTCTGCGTGTGTTGGTCTCGC 1533
Db 1708843 CGCACCGTCTCGAGTCTGCGTGTGTTGGTCTCGC 1708875
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RESULT 4

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US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
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; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match 100.0%; Score 1533; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTCAGCTCCGGAACCTTCGATCCCGAGGACCTCGAAATCCCATGCGCGCGAACCCGACC 60
Db 1707214 ATGTTTCAGCTCCGGAACCTTCGATCCCGAGGACCTCGAAATCCCATGCGCGCGAACCCGACC 1707273
QY 61 GCGTACCGCGCTTCCAGCAGCGCGACATCGCGCAGCGTAGTGGCTCTTTGTCCCGCGGA 120
Db 1707274 GCGTACCGCGCTTCCAGCAGCGCGACATCGCGCAGCGTAGTGGCTCTTTGTCCCGCGGA 1707333
QY 121 AAGACGCTTTCAGAGATCCCGCGCGCGAGATGAACAGGACGATTCGCTTAACGTGCGC 180
Db 1707334 AAGACGCTTTCAGAGATCCCGCGCGCGAGATGAACAGGACGATTCGCTTAACGTGCGC 1707393
QY 181 GAGGACTCCGCTATCGTCAAGGTTCCGTCGTCGAGCGGAACGTTGTGGCGGTGAATTGT 240
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QY 241 ACCGCGCGCGCGAATGTTCTGTGTCATCACTTGGTTAGCCCCCTTCGCGCTGCTCTGGG 300
Db 1707454 ACCGCGCGCGCGAATGTTCTGTGTCATCACTTGGTTAGCCCCCTTCGCGCTGCTCTGGG 1707513
QY 301 TTTTGTGCAATGTCAGGCTCGACAGCGCGCTCGAGCGCGGAGGCCACACATCCACGA 360
Db 1707514 TTTTGTGCAATGTCAGGCTCGACAGCGCGCTCGAGCGCGGAGGCCACACATCCACGA 1707573
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Db 1707694 TTTTCTGCAAGCGCGCGCGCTTCGCGCGCTCGGACGTTGGCGATCTCGCGAAGGATCC 1707753
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QY 661 CCACCTGGTGTGCGACATGCTTGGCGGTGCGGCGATACAGCGCATGCTGTGCGGGCA 720
Db 1707874 CCACCTGGTGTGCGACATGCTTGGCGGTGCGGCGATACAGCGCATGCTGTGCGGGCA 1707933
QY 721 ACATGCGCATGTCGCCATCACCGGTGCGCGGACGTGCGAGATACCAAGTCCAGGGGCATGA 780
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QY 781 CGTCGCGCAGGAATGTCGTGTCGTCGAGCGGACGTCACGCGCGAGTTGGTCTGGA 840
Db 1707994 CGTCGCGCAGGAATGTCGTGTCGTCGAGCGGACGTCACGCGCGAGTTGGTCTGGA 1708053
QY 841 TGAAGTTTCATCAAGATCAACGATCCAGGCTCAAAGTTGCCCCCGCACCCCGAGCCGGGGGA 900
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Db 1708054 TGAAGTTTCATCAAGATCAACAGCATCAGAGTCAAGTTGCCCCCAGCCCGAACCAGCGGGGA 1708113
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Db 1708114 ACTTCGAGTCTCTGGGATGCGCGTCTCCATATCACTCGGACGGGATGGAAGCACACCG 1708173
Qy 961 TCCTCTTGGGGTCCGGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1020
Db 1708174 TCCTCTTGGGGTCCGGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1708233
Qy 1021 AGTAGTCTCCGCTCGCAACACGCGATGTAATGCGCGAGCGGCGGACAGGCGCGCG 1080
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Db 1708594 CTGTGCGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGAGTACGCGCACGCT 1708653
Qy 1441 GCGAAGTATAGCGAGGTCGACTGAGCTTGGGCTCGAACCGCGTGGCGCGGTTGGG 1500
Db 1708654 GCGAAGTATAGCGAGGTCGACTGAGCTTGGGCTCGAACCGCGTGGCGCGGTTGGG 1708713
Qy 1501 CGCACGCTTCGAGTCTGGTCTGGTTGGCTCGC 1533
Db 1708714 CGCACGCTTCGAGTCTGGTCTGGTTGGCTCGC 1708746

RESULT 5

US-09-894-844-53/c
; Sequence 53, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-53

Query Match 73.0%; Score 1119; DB 3; Length 1119;
Best Local Similarity 100.0%; Pred. No. 3,6e-234; Indels 0; Gaps 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 377 CGTGGCGGCGGAGGTTGGCCACTTGGGTCCTTGAAGCGCGCGCGGCGGTTCGCGCGCG 436
Db 1059 CGTGGCGGCGGAGGTTGGCCACTTGGGTCCTTGAAGCGCGCGCGGCGGTTCGCGCGCG 1000
Qy 437 GTGCTCAGCGCGCATCGCGATCGCGGATCGCGGATCGCGGATCGCGGATCGCGGATCG 940
Db 999 GTGCTCAGCGCGCATCGCGATCGCGGATCGCGGATCGCGGATCGCGGATCGCGGATCG 940
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Db 759 CATGCTTGGGGTTCGCGCGATACACGCGCATGTTGGGCAACATGCGCATGTCGCC 700
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Db 699 ATGACCGCGTTCGCGCATGTCAGATPACAGTTCAGGGGATGACGTTCGCGAGAAATGTC 640
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Db 459 GTGAGGATGCGAGCTGTTGCTTAGCTTCAGCGGATCGATCCAGTTCGTTCCGCTC 400
Qy 1037 GCACAAACGCGATCTACTTCGCGCGAGCGCGCGAGCGCGCGTTCAGGTTTCATTTGAG 1096
Db 399 GCACAAACGCGATCTACTTCGCGCGAGCGCGCGAGCGCGCGTTCAGGTTTCATTTGAG 340
Qy 1097 GCGAGGTTTTCGTTCTTGAAGATCGCGCGGAAACAGTTCGCGGTACCGTTCGCGGTACTC 1156
Db 339 GCGAGGTTTTCGTTCTTGAAGATCGCGCGGAAACAGTTCGCGGTACCGTTCGCGGTACTC 280
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Db 279 ACAGATGATCGCGGGGTGGCATCGGTTCAGCGGCTTCGCGGACGATGATCTCCACCGG 220
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QY 712 TGTGGGCAACATGGCGATGTCGATGACCGGTCGCGAGTGCAGATACCACTCCA 771
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Db 1711314 GATCGTCCAGTAATCGTCCGCTTCGCACAGTCCGAGGTACTCGCCACGAGCGGCGGACA 1711255
QY 1072 GGGCGCGGTCAGTTCCTCCATTCAGCGCGAGGTTTTCGGTCTGGAAGATCGGCGGGAACA 1131
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Db 1711194 GCTGGGATAGCGGGGCGTACTCTCTATGATCTCGGGTGGGTCGTTGAGGCGAT 1711135
QY 1192 CGTGGGTCAGATGATCTCACCGGAAGTCTGTTGCTGCTGCGAAGAGCTGTCGAAGG 1251
Db 1711134 CGTACGATGATCACTCGACGGGAATCTCGGTCCTCTCGGGCGGGAAGCGCTCCAGG 1711075
QY 1252 CTTGACGGGTCAGCGCGCTGCTGAGTGTGCGAGCGATGCTCACTTGGGGCAA 1310
Db 1711074 CTTGCGAATGTAATCTCTCTGTTGTTAGAGATGAGAGATCACTCACTTGGGGCAA 1711016

RESULT 8

US-09-894-844-52/c

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 20.3%; Score 311; DB 3; Length 894;

; Sequence 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 311; Query Match 20.3%; Score 311; DB 3; Length 894;

; Sequence 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 311; Query Match 20.3%; Score 311; DB 3; Length 894;

Db 311 ATGTTTCAGCTCGGAACCTCGATCCGAGGACCTGAATCCCATGCGCGCAACCCGACC 252
QY 61 GGTATCCCGCTTCCAAAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 120
Db 251 GGTATCCCGCTTCCAAAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 192
QY 121 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTCGCG 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTCGCG 132
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGCGGAACGTTGTGGCGGTGAATTGT 240
Db 131 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGCGGAACGTTGTGGCGGTGAATTGT 72
QY 241 ACCGCGCGCGCGAATGTTCTGTGCCATCACTTGTAGCCCTTCGGCTGCTCTGGG 300
Db 71 ACCGCGCGCGCGAATGTTCTGTGCCATCACTTGTAGCCCTTCGGCTGCTCTGGG 12
QY 301 TTTGTGACAT 311
Db 11 TTTGTGACAT 1

RESULT 9

US-09-894-844-127/c

; Sequence 127, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 127

; LENGTH: 1236

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-127

Query Match

Best Local Similarity 3.7%; Score 56; DB 3; Length 1236;

; Sequence 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

; Sequence 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

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Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

Matches 86; Query Match 3.7%; Score 56; DB 3; Length 1236;

```
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2466
; LENGTH: 1574
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2466

Query Match          3.7%; Score 56; DB 3; Length 1574;
Best Local Similarity 47.1%; Pred. No. 0.0052;
Matches 241; Conservative 0; Mismatches 265; Indels 6; Gaps 2;

QY 355 CCACGAGCCCCCTGCGGCTCGCGGTCGCGGCGCGGCGGAGCTTGGCCCACTGGGTCTTGAGCC 414
DB 1224 CCACCACCGCTCTGCGCGCCCTTCATGTCCGATGACCTTGGCGCACCTGG-----GCGGC 1170

QY 415 GCGGCGGGGTCTGCGCCCGCGGTCTGTGAGCGCGGATGCGATGCCGATGCCGCG 474
DB 1169 GACGGCGGATCAACCGCGCGGTG-GGCTCGTCAGGAGCAACGCGCGGCTGCCCA 1111

QY 475 CGATGTTTCTGTCAGCGCGCGCCCTTCGCGGCTGGAACGTTGGCGATCTGGCGAA 534
DB 1110 TGAGGCGCTTGGGCCATGGCGCGCGCTTGGCCCATGCGGTGGCTGAGCGCTGTGTGGA 1051

QY 535 GATCAGTCGCGCCATGACGCGGATGAGTCTCTCGCGCGCGGGTCTCCGCGGAACAGT 594
DB 1050 CGTTTCAGGCGCTCCATAGGCGCCACCTTGTTCAGGCGCTTCGCGCGCTCACGCTCCGGCT 991

QY 595 CGAGCATCGCTCAACAGTCGCGCGGATGCCCGGACCTTCGCTCAACAGAACTTTGGCG 654
DB 990 CGGCCAGGCGGACAGCGCGGCCAGTATCATAGCAGCGCGGCCACTTCCAGCGCGGG 931

QY 655 GTTCCACCACTGGTTGTCACATGCTTGGCGGTCGCGGCGATACACGCGCATGGTGT 714
DB 930 GCAGCACCGCTCTGCGGCGAGCGCGCCAGCGCGCCCTTCAGGGCGCGCGGTGGTGG 871

QY 715 CCGGCAACATGCGGATGTCCCATGCACCGCTGCGGAGCTGCAGATACAGTCCAGG 774
DB 870 GGTCCACATCCATGACCTTTAGCGAGCCCTTCGAGCGGCTAGAGGTAGCGCACATCATGG 811

QY 775 GCATGACGTCGCGGAAATGTCTGTAGCGCTCGAGGCGAGCTACGCGCGGAGTTGG 834
DB 810 AGAAGTGTCTCTTGGCGCGCGCTTGGGCGCGATGAGCGCGTACACCGCGCCCTTGG 751

QY 835 TCTGGATGAAGTTTCATCAAGATCAACGCATCC 866
DB 750 GCACGAGAGCTGACCGCGTTGACGCGGACC 719

RESULT 11
US-09-902-540-1109
; Sequence 1109, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 953
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-953

Query Match          3.5%; Score 54.4; DB 3; Length 9521;
Best Local Similarity 43.0%; Pred. No. 0.015;
Matches 433; Conservative 0; Mismatches 566; Indels 9; Gaps 3;

; SEQ ID NO 1109
; LENGTH: 14077
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1109

Query Match          3.7%; Score 56; DB 3; Length 14077;
Best Local Similarity 47.1%; Pred. No. 0.0073;
Matches 241; Conservative 0; Mismatches 265; Indels 6; Gaps 2;

QY 355 CCACGAGCCCCCTGCGGCTCGCGGTCGCGGCGCGGAGCTTGGCCCACTGGGTCTTGAGCC 414
DB 6399 CCACCACCGCTCTGCGCGCCCTTCATGTCCGATGACCTTGGCGCACCTGG-----GCGGC 6453

QY 415 GCGGCGGGGTCTGCGCCCGCGGTCTGTGAGCGCGGATGCGATGCCGATGCCGCG 474
DB 6454 GACGCGCGGATCCAAACCGCGCGGTG-GGCTCGTCAGCAGACCAACGCGCGGCTGCCCA 6512

QY 475 CGATGTTTCTGTCAGCGCGCGCCCTTCGCGGCTGGAACGTTGGCGATCTGGCGAA 534
DB 6513 TGAGGCGCTTGGGCCATGGCGCGCGCTTGGCCCATGCGGTGGCTGAGCGCTGTGTGGA 6572

QY 535 GATCAGTCGCGCCATGACGCGGATGAGTCTCTCGCGCGCGGGTCTCCGCGGAACAGT 594
DB 6573 CGTTTCAGGCGCTCCATGAGGCCACCTTGTTCAGGCGCTTCGCGCGCTCACGCTCCGGCT 6632

QY 595 CGAGCATCGCTCAACAGTCGCGCGGATGCCCGGACCTTCGCTCAACAGAACTTTGGCG 654
DB 6633 CGGCCAGGCGCGGACGCGCGCCAGTATCATAGCAGCGCGGCCACTTCCAGCGCGGGCG 6692

QY 655 GGTCCACCACTGGTTGTGCCACATGCTTGGCGCTTGGCGGATACACGCGCATGGTGT 714
DB 6693 GCAGCACCGCTCTGCGGCGAGCGCGCCAGCGCGCCCTTCAGGGCGCGCGGTGGTGG 6752

QY 715 CCGGCAACATGCGGATGTGCCATGCACCGCTGCGGAGCTGCAGATACAGTCCAGG 774
DB 6753 GGTCCACATCCATGACCTTTCAGCGAGCCCTTCGAGCGGCTAGAGGTAGCGCACATCATGG 6812

QY 775 GCATGACGTCGCGGAAATGTCTGTAGCGCTTCGAGGCGAGCTACACGCGCGGAGTTGG 834
DB 6813 AGAAGTGTCTCTTGGCGCGCGCTTGGGCGCGATGAGCGCGCTACACCGCGCCCTTGG 6872

QY 835 TCTGGATGAAGTTTCATCAAGATCAACGCATCC 866
DB 6873 GCACGAGAGCTGACCGCGTTGACGCGGACC 6904

RESULT 12
US-09-902-540-953
; Sequence 953, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 953
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-953
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 89..2047
; US-09-385-707-4

Query Match 3.5%; Score 53; DB 3; Length 2155;
Best Local Similarity 48.0%; Pred. No. 0.025;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGCTCGAGCGGGAGGGCCACATCCACGAGCCCCCTCGGCTCGGC- 377
Db |||||
QY 1588 CTGCTCTCGGCGTGGGAAGACGGCGCGCCAGCGCGCCCACTCGCCGTCGGGGCTGCA 1529
Db |||||
QY 378 -GTCGGGGGGCGAGCTTGGCGCACCTGGGTCCTTGAGCGCGCGCGGGGTGTCGCCCGCGG 436
Db |||||
QY 1528 GAGCCCCGTTGTCCAGGTAGCGCGTACGTAGACGAGCCCGGGCGCCCGGGGGCACCCCGCG 1469
QY 437 GTGCTGCAGCGCCAGCATGCGGATCGGGGATGGCGCGATGCTTTCTTCGACAGCGCGC 496
Db |||||
QY 1468 CAGCCGAGGGTCACCGGACGCTGCGGTTGGGGTGGCGCGGGGTGTCGTCTCGCGTA 1409
QY 497 GCGCCCCCTCGGGCTCGGAACGTTGGCGATCTGGCGAAGATCCAGTCGGCCATGACGGC 556
Db |||||
QY 1408 GATCAGCACCGCGCGCGCCAGGCGTCGGCCGGGCCCTGGGGGGGTGGGCGCTGGCCAG 1349
QY 557 GATGAGTCTCTCGCGCGCGGGGTCTCCCGGGAAACAGTTCAGCATCGCGTCAAAACGTGCG 616
Db |||||
QY 1348 GACGCCACCGTGTGTTGTGTCCAGGACGCTCCCGGCTGGCGACACTTCGGGCCAGAG 1289
QY 617 CGCATGCCCGGACCCCTGCGTCAACAGAACTTTGGCGGTCACACCTGGTTGTGCCA 676
Db |||||
QY 1288 CTGCTCTTCATCCAGAGCGCCAGAGCCCATGGCCGTGAGCACCGGCTTGGCGAACAG 1229
QY 677 CATGCCCTTGGGCGTGGCGG 695
Db |||||
QY 1228 CTCACGTGCGGGGCGG 1210

Search completed: February 19, 2006, 20:42:30
Job time : 309.179 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 01:31:10 ; Search time 1317.13 Seconds
(without alignments)
9624.692 Million cell updates/sec

Title: US-09-673-476-1_COPY_11200_12800
Perfect score: 1533
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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1533	100.0	12732	6	US-10-259-678-1
2	1122	73.2	1122	7	US-10-282-122A-28775
3	1119	73.0	1119	3	US-09-894-844-53
4	1119	73.0	1119	7	US-10-388-902-53
5	1119	73.0	1119	7	US-10-647-089-53
6	479.8	31.3	1074	7	US-10-282-122A-28776
7	415.2	27.1	1023	7	US-10-282-122A-25931
8	311	20.3	894	3	US-09-894-844-52
9	311	20.3	894	7	US-10-388-902-52
10	194.4	12.7	366	7	US-10-647-089-52
11	194.4	12.7	366	7	US-10-282-122A-26084
12	104.8	6.8	276	7	US-10-388-902-127
13	72.8	4.7	951	7	US-10-282-122A-13587
14	65.2	4.3	1395	7	US-10-282-122A-35893
15	57.4	3.7	8421	3	US-09-976-059-1
16	56	3.7	1236	3	US-09-894-844-127
17	56	3.7	1236	7	US-10-388-902-127
18	56	3.7	1236	7	US-10-647-089-127
19	56	3.7	1236	8	US-10-481-265-6
20	55.6	3.6	1544	7	US-10-437-963-7661
21	55.2	3.6	1296	6	US-10-329-027-11
22	54.8	3.6	2196	6	US-10-156-761-5077
23	54.8	3.6	2517	7	US-10-282-122A-25466

ALIGNMENTS

RESULT 1

US-10-259-678-1

; Sequence 1, Application US/10259678

; Publication NO. US20030198974A1

; GENERAL INFORMATION:

; APPLICANT: Cole, Stewart

; APPLICANT: Buchrieser-Brosch, Roland

; APPLICANT: Gordon, Stephen

; APPLICANT: Billault, Alain

; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

; FILE REFERENCE: 3495-0169

; CURRENT APPLICATION NUMBER: US/10/259,678

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/060,756

; PRIOR FILING DATE: 1998-04-16

; NUMBER OF SEQ ID NOS: 743

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 12732

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-10-259-678-1

Query Match 100.0%; Score 1533; DB 6; Length 12732;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 ATGTTTCAGCTCGCAACCTCGATCCGAGGACCTGAAATCCCATCGCGGACCCGACC 60

DB

11200 ATGTTTCAGCTCGCAACCTCGATCCGAGGACCTGAAATCCCATCGCGGACCCGACC 11259

QY

61 GCGTACCCGCTTCCAAGCAGCCGACATCGCGCAGCGTAGTGGCTCTTTGCCCGGGA 120

DB

11260 GGTACCCGCTTCCAAGCAGCCGACATCGCGCAGCGTAGTGGCTCTTTGCCCGGGA 11319

QY

121 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGGCG 180

DB

11320 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGGCG 11379

QY

181 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCGAGCGGACGTTGTGGGGGGTGAATTGT 240

DB

11380 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCGAGCGGACGTTGTGGGGGGTGAATTGT 11439

QY

241 ACCGCGCGCGCGGAATGTTCTTCGTGTCATCACTTGGTTAGCCCTTCCTGCTGCTGCTGGG 300

Db 11440 ACCGGCCGCGCGAATGTTCTGTGCGCATCACTTGGTTAGCCCTTTCGGCTCGTCTCGG 11499
QY 301 TTGTGCGACATGGTTCAGGCTCGACAGCCGCGTGGAGCCGGAGGCCACACATCCACGA 360
Db 11500 TTGTGCGACATGGTTCAGGCTCGACAGCCGCGTGGAGCCGGAGGCCACACATCCACGA 11559
QY 361 GCGCCCTCGGGCTCGGCGTGGCGCGCGGCGAGCTTGGCCACCTGGGTCTTTGAGCCGCGCG 420
Db 11560 GCGCCCTCGGGCTCGGCGTGGCGCGCGGCGAGCTTGGCCACCTGGGTCTTTGAGCCGCGCG 11619
QY 421 CGGGTGTGCGCCCGCGGTCTCGAGCGCCAGCATGCGGGATCGCGCGATGG 480
Db 11620 CGGGTGTGCGCCCGCGGTCTCGAGCGCCAGCATGCGGGATCGCGCGCGATGG 11679
QY 481 TTTCCTGCGAGCGCGCGCCCTCTCGGGCTTGGAACTGTTGGCGATCTCGCGAAGGATCC 540
Db 11680 TTTCCTGCGAGCGCGCGCCCTCTCGGGCTTGGAACTGTTGGCGATCTCGCGAAGGATCC 11739
QY 541 AGTCGCGCATGACGGGATGAGCTCTCTCGCGCGCGGGTCTCCCGGAAACAGGTCGAGCA 600
Db 11740 AGTCGCGCATGACGGGATGAGCTCTCTCGCGCGCGGGTCTCCCGGAAACAGGTCGAGCA 11799
QY 601 TCGCGTCAAACGTCGCGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGTCCA 660
Db 11800 TCGCGTCAAACGTCGCGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGTCCA 11859
QY 661 CCACCTGGTGTGCCACATGCCCTTGGCGGTGGCGGATACACGGGCATGGTGTGGGCA 720
Db 11860 CCACCTGGTGTGCCACATGCCCTTGGCGGTGGCGGATACACGGGCATGGTGTGGGCA 11919
QY 721 ACATGCGATGTCGCATGCGATGCGCGTGGCGGATGCGGATACCGTCCAGGGGATGA 780
Db 11920 ACATGCGATGTCGCATGCGCGTGGCGGATGCGGATACCGTCCAGGGGATGA 11979
QY 781 CGTCGCGAGGAATGCTGTAGCGCTCGAGCGAGGTACACGCGCGAGTTGCTCGA 840
Db 11980 CGTCGCGAGGAATGCTGTAGCGCTCGAGCGAGGTACACGCGCGAGTTGCTCGA 12039
QY 841 TGAAGTTCAATCAAGATCAACGATCAAGCTCAAGTTGCCCGCGACCCCGAACCAGGGGGA 900
Db 12040 TGAAGTTCAATCAAGATCAACGATCAAGCTCAAGTTGCCCGCGACCCCGAACCAGGGGGA 12099
QY 901 ACTTGAGTCTTGGCATGGCGCTCTCCATATACCTCGAGCGGATGGAAGCACACCG 960
Db 12100 ACTTGAGTCTTGGCATGGCGCTCTCCATATACCTCGAGCGGATGGAAGCACACCG 12159
QY 961 TCGTCTTGGGGTGGCGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1020
Db 12160 TCGTCTTGGGGTGGCGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 12219
QY 1021 AGTAGTCTGCTCGCATCAACGCGACGTACTCTCGCGAGCGCGCGACAGGGCGCGG 1080
Db 12220 AGTAGTCTGCTCGCATCAACGCGACGTACTCTCGCGAGCGCGCGACAGGGCGCGG 12279
QY 1081 TCAGTTTCCATGAGCGCGAGTTTTCGGTCTGGAAGATCGCGCGGAAACAGTTCGGGT 1140
Db 12280 TCAGTTTCCATGAGCGCGAGTTTTCGGTCTGGAAGATCGCGCGGAAACAGTTCGGGT 12339
QY 1141 ACCGCTCGGCGTACTACCGGATGATCGCGGGGTGCGATCGGTTCGACGCGTCTCGGCGA 1200
Db 12340 ACCGCTCGGCGTACTACCGGATGATCGCGGGGTGCGATCGGTTCGACGCGTCTCGGCGA 12399
QY 1201 CGATGATCTCCACCGGGAAGTCGGTTTGTGCTCGAGAAAGCTGTGGAAGGCTTCACCGG 1260
Db 12400 CGATGATCTCCACCGGGAAGTCGGTTTGTGCTCGAGAAAGCTGTGGAAGGCTTCACCGG 12459
QY 1261 CGTAGCCCGCTGTTGTGAGTGTGAGACATGCTACCTTGGGGGAAAGCTGGGGAC 1320
Db 12460 CGTAGCCCGCTGTTGTGAGTGTGAGACATGCTACCTTGGGGGAAAGCTGGGGAC 12519
QY 1321 TCACCGTGGCGCTTTTCTGTCGCGGCGCAAGGGTATTGCGATGCGCAACCTGTAATCGC 1380

Db 12520 TCACCGTGGCGCTTTTCTGTCGCGCGCGAAGGGTATTGCGATGCGAAACGTGAATCGC 12579
QY 1381 CTGTGCGCCCGCGCGCTCGGCGCTGTCGTCCTGTGGTTCGGCGGAGCTACGGCACACGCT 1440
Db 12580 CTGTGCGCCCGCGCGCTCGGCGCTGTCGTCCTGTGGTTCGGCGGAGCTACGGCACACGCT 12639
QY 1441 GCGAAGTATACGAGGGTGCACTGACGTTGGCTCGAAACCGCTGGCGCGGTCGTGGG 1500
Db 12640 GCGAAGTATACGAGGGTGCACTGACGTTGGCTCGAAACCGCTGGCGCGGTCGTGGG 12699
QY 1501 CGCACCGTCTCGAGTCGGTCTGGTTCGGCTCGC 1533
Db 12700 CGCACCGTCTCGAGTCGGTCTGGTTCGGCTCGC 12732

RESULT 2
US-10-282-122A-28775/c
; Sequence 28775, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28775
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28775

Query Match 73.2%; Score 1122; DB 7; Length 1122;
Best Local Similarity 100.0%; Pred. No. 1.9e-296;
Matches 1122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 314 TCAGGCTCGACAGCCGCTCGGAGCGGAGGCCACACATCCAGAGCCCTCGGGCT 373
Db 1122 TCAGGCTCGACAGCCGCTCGGAGCGGAGGCCACACATCCAGAGCCCTCGGGCT 1063


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QY 374 CGGCGTCCGGCGGCGAGCTTGCGCCACTGGGCTTTAGAGCCGCGCGGGTGTGCCCC 433
Db 1062 CGGCGTCCGGCGGCGAGCTTGCGCCACTGGGCTTTAGAGCCGCGCGGGTGTGCCCC 1003
QY 434 GCGGTCTGAGCCAGCCAGCATGCGGATCCGGGATGCGCGCATGGTTCTTGAGCGC 493
Db 1002 GCGGTCTGAGCCAGCCAGCATGCGGATCCGGGATGCGCGCATGGTTCTTGAGCGC 943
QY 494 GCGCGCCCTCCGGGCTTGGAACCTTGCGGATCTGCGAAGGATCCAGTCGCGCATGAC 553
Db 942 GCGCGCCCTCCGGGCTTGGAACCTTGCGGATCTGCGAAGGATCCAGTCGCGCATGAC 883
QY 554 GCGGATGAGCTCTCGCGCGCGGGTCTCCCGGGAACAGGTCCAGCATCGCGTCAAAAGT 613
Db 882 GCGGATGAGCTCTCGCGCGCGGGTCTCCCGGGAACAGGTCCAGCATCGCGTCAAAAGT 823
QY 614 GCGCGATGCCCGGAGCCCTGCGTCAACAGAACTTTGGGGGTCCACACCTGGTTGG 673
Db 822 GCGCGATGCCCGGAGCCCTGCGTCAACAGAACTTTGGGGGTCCACACCTGGTTGG 763
QY 674 CCACATGCTTGGGCGTGGCGGCGATACACGGCATGGTGTGCGGCAACATGGCGATGTC 733
Db 762 CCACATGCTTGGGCGTGGCGGCGATACACGGCATGGTGTGCGGCAACATGGCGATGTC 703
QY 734 GCCATGACCGGTGCGGACGTGCGAGATACCAATCCAGGGGATGACGTCCGAGGAAT 793
Db 702 GCCATGACCGGTGCGGACGTGCGAGATACCAATCCAGGGGATGACGTCCGAGGAAT 643
QY 794 GTGCTGTAGCGTCCAGGCGAGGTACACGGCGGAGTTGGTCTGATGAGTTGATCAA 853
Db 642 GTGCTGTAGCGTCCAGGCGAGGTACACGGCGGAGTTGGTCTGATGAGTTGATCAA 583
QY 854 GATCAACGATCCAGGCTCAAGTTGCGCGCACCCGAAACCGGGGGAACCTTCGAGTCCCTT 913
Db 582 GATCAACGATCCAGGCTCAAGTTGCGCGCACCCGAAACCGGGGGAACCTTCGAGTCCCTT 523
QY 914 GGCATGGCGTCTCCCATATACATCGAGCGGATGGAAGCACACGTCGTCTTGGGGTG 973
Db 522 GGCATGGCGTCTCCCATATACATCGAGCGGATGGAAGCACACGTCGTCTTGGGGTG 463
QY 974 CCGGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCCAGTGTGTCGCG 1033
Db 462 CCGGTTCAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCCAGTGTGTCGCG 403
QY 1034 CTCGCACAAACGCGACGTACTCGCGGAGCGGCGGACAGGCGCGGTTCAGGTTCCCAT 1093
Db 402 CTCGCACAAACGCGACGTACTCGCGGAGCGGCGGACAGGCGCGGTTCAGGTTCCCAT 343
QY 1094 GAGCCGAGGTTTTTCGGTCTGGAAGATCGGCGGAAACAGTGTGCGGTAACGCTCGGCGTA 1153
Db 342 GAGCCGAGGTTTTTCGGTCTGGAAGATCGGCGGAAACAGTGTGCGGTAACGCTCGGCGTA 283
QY 1154 CTCACGGAATGATCGCGGGGTGCGATCGGTTCGACGCGTGTGCGGCAACGATGATCTCCAC 1213
Db 282 CTCACGGAATGATCGCGGGGTGCGATCGGTTCGACGCGTGTGCGGCAACGATGATCTCCAC 223
QY 1214 CCGGAAGTCGTTGCTGCGAAGCTGTGCGAAGCTGTGCGGCGTGTGCGGCGTGTGCGGCGT 1273
Db 222 CCGGAAGTCGTTGCTGCGAAGCTGTGCGAAGCTGTGCGGCGTGTGCGGCGTGTGCGGCGT 163
QY 1274 GTTGTGAGTGGTTCGAGACGATGCTCACTTTGGGGCAAGCTGGGGACTCACCGTCCGGCC 1333
Db 162 GTTGTGAGTGGTTCGAGACGATGCTCACTTTGGGGCAAGCTGGGGACTCACCGTCCGGCC 103
QY 1334 TTTTCTGCGCGCGCGCAAGGATTTGCGATGCGGAAACGTGATCCCTGTGTCGCGCGCG 1393
Db 102 TTTTCTGCGCGCGCGCAAGGATTTGCGATGCGGAAACGTGATCCCTGTGTCGCGCGCG 43
QY 1394 CCGTCCGCGCGTGTGCGCTGTTGGTCCGCGGAGGTACGGCAC 1435
Db 42 CCGTCCGCGCGTGTGCGCTGTTGGTCCGCGGAGGTACGGCAC 1
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RESULT 3

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US-09-894-844-53/c
; Sequence 53, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-53
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Query Match 73.0%; Score 1119; DB 3; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.3e-295;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 GGCTGCACAGCCGCTCGGAGCGGGGCGGCACACATCCAGAGCCCTCGCGGTCCG 376
Db 1119 GGCTGCACAGCCGCTCGGAGCGGGGCGGCACACATCCAGAGCCCTCGCGGTCCG 1060
QY 377 CGTCCGCGCGGCGAGCTTCGCCACATGCGGTCTTGAGCGCGCGCGGGTGTGCGCCGCG 436
Db 1059 CGTCCGCGCGGCGAGCTTCGCCACATGCGGTCTTGAGCGCGCGCGGGTGTGCGCCGCG 1000
QY 437 GTGCTGCACGCCAGCATGCGGATCGGCGGATGCGCGGATGCGGTTCCTGACGCGCG 496
Db 999 GTGCTGCACGCCAGCATGCGGATCGGCGGATGCGCGGATGCGGTTCCTGACGCGCG 940
QY 497 GCGCCCTCCGGGCTTGGAACGTTGCGCATCTGCGGAAGGATCCAGTCGSCCATGACGCG 556
Db 939 GCGCCCTCCGGGCTTGGAACGTTGCGCATCTGCGGAAGGATCCAGTCGSCCATGACGCG 880
QY 557 GATGAGCTCTCGCGCGCGGGTCTCCCGGGAACAGGTTCAGCATCGCGTCAAAAGTTCG 616
Db 879 GATGAGCTCTCGCGCGCGGGTCTCCCGGGAACAGGTTCAGCATCGCGTCAAAAGTTCG 820
QY 617 CGCATGCCCGGACCTGCGTCAACAGAACTTTGGGGGTCCACACCTGGTGTGCGCA 676
Db 819 CGCATGCCCGGACCTGCGTCAACAGAACTTTGGGGGTCCACACCTGGTGTGCGCA 760
QY 677 CATGCTTCGGGCTGCGCGCGATACACGCGCATGCGTTCGGGCAACATGCGCATGTCGCG 736
Db 759 CATGCTTCGGGCTGCGCGCGATACACGCGCATGCGTTCGGGCAACATGCGCATGTCGCG 700
QY 737 ATGCAACCGCGTCCCGGACGTGAGATACAGTTCAGGGGATGACGTTCGCGAGGAATGTC 796
Db 699 ATGCAACCGCGTCCCGGACGTGAGATACAGTTCAGGGGATGACGTTCGCGAGGAATGTC 640
QY 797 GTGCTAGCGCTCGAGCGGACGATACACGCGCGGATGCGGTTCGATGAAGTTCATCAGAT 856
Db 639 GTGCTAGCGCTCGAGCGGACGATACACGCGCGGATGCGGTTCGATGAAGTTCATCAGAT 580
QY 857 CAAACGATCCAGGCTCAAGTTGCCCGCACCCCGAACCGGGGGAACTTCGAGTCTTGGC 916
Db 579 CAAACGATCCAGGCTCAAGTTGCCCGCACCCCGAACCGGGGGAACTTCGAGTCTTGGC 520
QY 917 ATGGCGGTCTCCCATATACATCGGACGGGATGGAAGCACACGTCGTCTTGGGGTCCG 976
Db 519 ATGGCGGTCTCCCATATACATCGGACGGGATGGAAGCACACGTCGTCTTGGGGTCCG 460
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QY 977 GTCGAGGAATCGACCTGTTTCTAGCTTACCGGATCGATCCAGTAGTCTCGCCCTC 1036
DB 459 GTCGAGGAATCGACCTGTTTCTAGCTTACCGGATCGATCCAGTAGTCTCGCCCTC 400
QY 1037 GCACAAACGCGAGTACTCGCCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 1096
DB 399 GCACAAACGCGAGTACTCGCCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 340
QY 1097 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGAACAACGTCGGGTACCGCTCGCGGTACTC 1156
DB 339 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGAACAACGTCGGGTACCGCTCGCGGTACTC 280
QY 1157 ACGGATGATCGCCGGGTGGCATCGGTCCAGCGGTCTCGGCGACGATCTCCACCGG 1216
DB 279 ACGGATGATCGCCGGGTGGCATCGGTCCAGCGGTCTCGGCGACGATCTCCACCGG 220
QY 1217 GAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACGGGTGATCCCGCTGGTT 1276
DB 219 GAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACGGGTGATCCCGCTGGTT 160
QY 1277 GTGAGTGTGCGAGACGATCTCACCTTGGGCGAAAGCTGGGACTCACCGTCGGCCCTTT 1336
DB 159 GTGAGTGTGCGAGACGATCTCACCTTGGGCGAAAGCTGGGACTCACCGTCGGCCCTTT 100
QY 1337 TCCTCGCGCGCGCGAAGGTATTGCGATGCGGAAAGCTGTAATCGCCTGTCGCCCGCGCGCG 1396
DB 99 TCCTCGCGCGCGCGAAGGTATTGCGATGCGGAAAGCTGTAATCGCCTGTCGCCCGCGCGCG 40
QY 1397 TCGGCGCTGTCGGCTGGTGTGCGGAGACGTACGSCAC 1435
DB 39 TCGGCGCTGTCGGCTGGTGTGCGGAGACGTACGSCAC 1

RESULT 4

US-10-388-902-53/c
; Sequence 53, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-53

Query Match 73.0%; Score 1119; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.3e-295;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 GCGTCGACGCGCGCTCGGAGCGGGAGCGGCACACATCCAGAGCCCTCGGCTCGG 376
DB 1119 GCGTCGACGCGCGCTCGGAGCGGGAGGGGCACACATCCAGAGCCCTCGGCTCGG 1060
QY 377 CGTCGCGCGCGCGAGCTTCGCGCACTGGGTCTTGAAGCCCGCGGGGTGTCGCCCGCG 436
DB 1059 CGTCGCGCGCGCGAGCTTCGCGCACTGGGTCTTGAAGCCCGCGGGGTGTCGCCCGCG 1000

RESULT 5

US-10-647-089-53/c
; Sequence 53, Application US/10647089

QY 437 GTGCTGCAGCGCAGCATGGCGATCGGGGATGGCGCGCGATGGTTTCTCTGAGCCCGCG 496
DB 999 GTGCTGCAGCGCAGCATGGCGATCGGGGATGGCGCGCGATGGTTTCTCTGAGCGCGCG 940
QY 497 GCGCCCTTCCGGCGCTGGAAAGTTCGCGATCTGGCGAAGGATCCAGTCGGCGCATGACGC 556
DB 939 GCGCCCTTCCGGCGCTGGAAAGTTCGCGATCTGGCGAAGGATCCAGTCGGCGCATGACGC 880
QY 557 GATGAGTCTCTCGCGCGCGGGGTCTCCCGGGAAACAGGTTCAGCATCGCGTCAAAAGTTC 616
DB 879 GATGAGTCTCTCGCGCGCGGGGTCTCCCGGGAAACAGGTTCAGCATCGCGTCAAAAGTTC 820
QY 617 CGCATGCCCGCGACCTTCGCTCAACAGAACTTTGGCGGGTCCACCACTGGTTGTGCCA 676
DB 819 CGCATGCCCGCGACCTTCGCTCAACAGAACTTTGGCGGGTCCACCACTGGTTGTGCCA 760
QY 677 CATGCTTTGGGCGTGGCGCGATACAGCGCATGGTGTGGGCAACATCGCGATGTCCGC 736
DB 759 CATGCTTTGGGCGTGGCGCGATACAGCGCATGGTGTGGGCAACATCGCGATGTCCGC 700
QY 737 ATGCAACCGCGTCCCGACGTGCAGATACAGTCCAGGGGCGATGACGTCCGCGAGGAATGTC 796
DB 699 ATGCAACCGCGTCCCGACGTGCAGATACAGTCCAGGGGCGATGACGTCCGCGAGGAATGTC 640
QY 797 GTGCTAGCGCTCGAGCGCGAGGTACAGCGCGAGTTGGTCTGGAAGAAGTTCATCAAGAT 856
DB 639 GTGCTAGCGCTCGAGCGCGAGGTACAGCGCGAGTTGGTCTGGAAGAAGTTCATCAAGAT 580
QY 857 CAACGCATCCAGGCTCAAGTTGCCCGCGCACCGAAACCGGGGGAACTTCGAGTCTTGGC 916
DB 579 CAACGCATCCAGGCTCAAGTTGCCCGCGCACCGAAACCGGGGGAACTTCGAGTCTTGGC 520
QY 917 ATGCGCGTCTCTCCATATCACTCGGACGGGATGGAAGCAACACGTCGTCTTGGGGTGGCG 976
DB 519 ATGCGCGTCTCTCCATATCACTCGGACGGGATGGAAGCAACACGTCGTCTTGGGGTGGCG 460
QY 977 GTGAGGAATGCGACTGTTTGTAGTTTACGCGGATCGATCCAGTAGTCTCGCCCTC 1036
DB 459 GTGAGGAATGCGACTGTTTGTAGTTTACGCGGATCGATCCAGTAGTCTCGCCCTC 400
QY 1037 GCACAAACGCGAGTACTCGCCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 1096
DB 399 GCACAAACGCGAGTACTCGCCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 340
QY 1097 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGAACAACGTCGGGTACCGCTCGCGGTACTC 1156
DB 339 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGAACAACGTCGGGTACCGCTCGCGGTACTC 280
QY 1157 ACGGATGATCGCCGGGTGGCATCGGTCCAGCGGTCTCGGCGACGATCTCCACCGG 1216
DB 279 ACGGATGATCGCCGGGTGGCATCGGTCCAGCGGTCTCGGCGACGATCTCCACCGG 220
QY 1217 GAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACGGGTGAGCCCGCTGGTT 1276
DB 219 GAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACGGGTGAGCCCGCTGGTT 160
QY 1277 GTGAGTGTGCGAGACGATCTCACCTTGGGCGAAAGCTGGGACTCACCGTCGGCCCTTT 1336
DB 159 GTGAGTGTGCGAGACGATCTCACCTTGGGCGAAAGCTGGGACTCACCGTCGGCCCTTT 100
QY 1337 TCCTCGCGCGCGCGAAGGTATTGCGATGCGGAAAGCTGTAATCGCCTGTCGCCCGCGCGCG 1396
DB 99 TCCTCGCGCGCGCGAAGGTATTGCGATGCGGAAAGCTGTAATCGCCTGTCGCCCGCGCGCG 40
QY 1397 TCGGCGCTGTCGGCTGGTGTGCGGAGACGTACGSCAC 1435
DB 39 TCGGCGCTGTCGGCTGGTGTGCGGAGACGTACGSCAC 1

Publication No. US20040063923A1
GENERAL INFORMATION:
APPLICANT: Behr, Marcel
APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of the M. Tuberculosis Complex
FILE REFERENCE: STAN102CON
CURRENT APPLICATION NUMBER: US/10/647,089
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US/09/894,844
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 1119
TYPE: DNA
ORGANISM: Mycobacteria tuberculosis
US-10-647-089-53

Query Match 73.0%; Score 1119; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.3e-295; Mismatches 0; Indels 0; Gaps 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	317	GGCTCGACAGCCGCTCGGAGCGGGAGGCGCACATCACAGAGCCCTCGGCTCGG	376
DB	1119	GGCTCGACAGCCGCTCGGAGCGGGAGGCGCACATCACAGAGCCCTCGGCTCGG	1060
QY	377	CGTCGGCGCGGAGCTTGGCCACCTGGGTTTTCAGCGCGCGCGGGTGTCCGCCCGG	436
DB	1059	CGTCGGCGCGGAGCTTGGCCACCTGGGTTTTCAGCGCGCGCGGGTGTCCGCCCGG	1000
QY	437	GTCTCGAGCGCAGATCGGATCGGCGGATCGGCGGATCGGTTTCTCGAGCGCGG	496
DB	999	GTCTCGAGCGCAGATCGGATCGGCGGATCGGCGGATCGGTTTCTCGAGCGCGG	940
QY	497	GGCCCTCGGGCTCGGAGCTTGGCGATCTGGCGAAGGATCCAGTCGGCCATGACGGC	556
DB	939	GGCCCTCGGGCTCGGAGCTTGGCGATCTGGCGAAGGATCCAGTCGGCCATGACGGC	880
QY	557	GATGAGCTCTCGCGCGGGTCTCCGGGAAACAGGTGAGCATCGGTCAAACGTGCG	616
DB	879	GATGAGCTCTCGCGCGGGTCTCCGGGAAACAGGTGAGCATCGGTCAAACGTGCG	820
QY	617	CGCATGCCCGGACCTGGCTCAACAGAACTTTGGCGGTCCACACCTGGTTGTGCCA	676
DB	819	CGCATGCCCGGACCTGGCTCAACAGAACTTTGGCGGTCCACACCTGGTTGTGCCA	760
QY	677	CATGCTTGGCGTGGCGCGATACACGCGCATGTCGGGCAACATGCGCATGTCGCC	736
DB	759	CATGCTTGGCGTGGCGCGATACACGCGCATGTCGGGCAACATGCGCATGTCGCC	700
QY	737	ATGACCGGTGCGGAGCTGCGAGATACAGTCACAGGGGATGACGTGCGGAGGAATGC	796
DB	699	ATGACCGGTGCGGAGCTGCGAGATACAGTCACAGGGGATGACGTGCGGAGGAATGC	640
QY	797	GTCTAGCGCTCGAGGCGGTGACCGCGGATGTTGTTGATGAAGTTTCATCAAGT	856
DB	639	GTCTAGCGCTCGAGGCGGTGACCGCGGATGTTGTTGATGAAGTTTCATCAAGT	580
QY	857	CAACGATCCAGGCTCAAGTTGCCCGCACCCGAGGAACTTCGAGTCTTGGC	916
DB	579	CAACGATCCAGGCTCAAGTTGCCCGCACCCGAGGAACTTCGAGTCTTGGC	520
QY	917	ATGGCGTCTCCCATATCATCTCGGAGCGGATGGAAGCACACCGTCTTGGGGTGGC	976
DB	519	ATGGCGTCTCCCATATCATCTCGGAGCGGATGGAAGCACACCGTCTTGGGGTGGC	460

QY	977	GTGAGGAATCGACCTGTTTCTAGCTTTCAGCGGATCGATCCAGTAGTGTGTCGCGCTC	1036
DB	459	GTGAGGAATCGACCTGTTTCTAGCTTTCAGCGGATCGATCCAGTAGTGTGTCGCGCTC	400
QY	1037	GCACACGCGAGCTACTCCCGCGAGCGCGCGAGCGCGCGGTTCAGGTTCCCATTTGAG	1096
DB	399	GCACACGCGAGCTACTCCCGCGAGCGCGCGAGCGCGCGGTTCAGGTTTCATTTGAG	340
QY	1097	GCGAGGTTTTCGTTCTTGAAGATCGCGCGAAACAGTCGCGGTACCGTTCGCGTACTC	1156
DB	339	GCGAGGTTTTCGTTCTTGAAGATCGCGCGAAACAGTCGCGGTACCGTTCGCGTACTC	280
QY	1157	ACGAGTATCGCGCGGTGCGCATCGGTGACGCGGTCTCGCGGACGATGATCTCCACCGG	1216
DB	279	ACGAGTATCGCGCGGTGCGCATCGGTGACGCGGTCTCGCGGACGATGATCTCCACCGG	220
QY	1217	GAGTCGTTGCTGTCGAGAAAGCTGCGAAGGCTGACGCGGTGACGCGGTAGCGCGCTGTT	1276
DB	219	GAGTCGTTGCTGTCGAGAAAGCTGCGAAGGCTGACGCGGTGACGCGGTAGCGCGCTGTT	160
QY	1277	GTGAGTGTGCGAGAGCATCTCACCTTGGGGCAAAAGCTGCGGACTCACCGTGGGCTTT	1336
DB	159	GTGAGTGTGCGAGAGCATCTCACCTTGGGGCAAAAGCTGCGGACTCACCGTGGGCTTT	100
QY	1337	TCTCGCGCGCGCAAGGTTTTCGATCGCGCAACGTAATCGCTGTGCGCGCGCGCG	1396
DB	99	TCTCGCGCGCGCAAGGTTTTCGATCGCGCAACGTAATCGCTGTGCGCGCGCGCG	40
QY	1397	TGCGCGCTGTCGCGCTGTTGTTGTCGCGGACGTCACGCGAC	1435
DB	39	TGCGCGCTGTCGCGCTGTTGTTGTCGCGGACGTCACGCGAC	1

RESULT 6
US-10-282-122A-28776/c
Sequence 28776, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308

Db 719 CCGGACCCCTGCATCCGCCAGAAAGGTGGCCGGATCGGTGATCGACTTGTACCAATGCGC 660
Qy 684 TGGGCGTGGCGGATACACGGCCATGGTTCGGGACACATCGCATGCGCATGACC 743
Db 659 CGCGGGTGGCGGATAGACCGGCATCGTCTCCGGCAGCATGCGCATGGCGCTTCGGCG 600
Qy 744 GCGTGGCGGACGTGCAGATACACAGTCCAGGGGATGACGTCCGCGAGAAATGTCGTCTAG 803
Db 599 GCATGCGGACGTGCAGGTACAGTCCAGGGGATGACATCGCGCGGATGTCGTCTAG 540
Qy 804 CGCTCGAGGCGACGGTACACGGCCGAGTGGTCTGATGAAGTTCATCAAGATCAACGCA 863
Db 539 CGGGGAGGCGCGGTACATACCGAGTGGTCTGATGAAGTTCGCGAGATCAGCGTC 480
Qy 864 TCCAGGCTCAAGTTCGCGCCGCCACCGGAGGCGGAGC----- 902
Db 479 TCGAAGCTGAGGTTCACCGCCCGAAAGGGCGCGGAAACTTTGGCGAGGAGATCTCTTCG 420
Qy 903 -----TTCGAGTTCCTTGGCATGGCGCTCTCCCATATC 935
Db 419 AACTTCGATACAGGTGTGGACGAGTTTCTCTCTCCGCGCATCTGTGGTTCAGACC 360
Qy 936 ACTCGACCGGATGGAAGCACACCGTCTTGGGGTGGCGGTTCGAGGAATGCGACTGT 995
Db 359 ACCTGCACCGGTGGAACACACCGTGTGTCGGGATCTTCGTCCAGCAAGCCACTTGT 300
Qy 996 TTGCTTAGCTTCAGCGATCGATCCAGTAGTCTCGCGCTCGCACAAAGGAGTACTCG 1055
Db 299 TTGGTCAGTTTCAACGGGTGCAGCCAGTAGTCTCGCGCTCGCACAGCGCATGTACTCG 240
Qy 1056 CCGCGAGCGCGCACAGGGCGCGGTTCAGTTCCCATGAGGCGGAGTTTTCGTCTCG 1115
Db 239 CCAGCGCGCGGACAGGGCACCGGTGAGTTCGCTTGAGGCGGAGTTTTCGACCGC 180
Qy 1116 AAGATCGCGCGGAACAGTTCGGGTACCGTTCGGGTCTACTCAGGATGATCGCGGGGTG 1175
Db 179 AGGATCGCGCGGAAGAGTTTCGATGCGGTTCGGGTCTACTCAGGATGATCGCGGGTGTG 120
Qy 1176 GCATCGGTGACCGCTGTCGGGACGATGATCTCCACCGGAGTTCGTTGCTGCTGTCG 1235
Db 119 GCATCGGTGAGGCATCGTTCGGGACGATGATCTCCATCGGAAAGTTCGACCGCTGGGG 60
Qy 1236 AGAAGCTGTCGAAGCCTGCAGCGGCTGACCGCGGTGAGTTCGTTGAGTTCGAGACGA 1293
Db 59 AGAAGCGGTCCAACGTTCGCGGACATAGGCTCTGTTGTTGGTGTGACACCA 2

RESULT 8
US-09-894-844-52/c
; Sequence 52, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-52

Query Match 20.3%; Score 311; DB 3; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75; Indels 0; Gaps 0;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC 60
Db 311 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC 252
Qy 61 GCGTACCCGCTTCGAGCAGCGGACATCGGCCAGCGGATGAGTGGCTCTTGTCTCCCGGGA 120
Db 251 GCGTACCCGCTTCGAGCAGCGGACATCGGCCAGCGGATGAGTGGCTCTTGTCTCCCGGGA 192
Qy 121 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTTAAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTTAAACGTGCGC 132
Qy 181 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTCGAGCGGAAACGTTGTGGCGGTGAATTGT 240
Db 131 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTCGAGCGGAAACGTTGTGGCGGTGAATTGT 72
Qy 241 ACGCGCGCGCGGATGTTCTGTCGATCATTGTTAGCCCTTCGCGTGTCTCTGGTCTCTGG 300
Db 71 ACGCGCGCGCGGATGTTCTGTCGATCATTGTTAGCCCTTCGCGTGTCTCTGGTCTCTGG 12
Qy 301 TTTGTCGACAT 311
Db 11 TTTGTCGACAT 1

RESULT 9
US-10-388-902-52/c
; Sequence 52, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-52

Query Match 20.3%; Score 311; DB 7; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75; Indels 0; Gaps 0;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC 60
Db 311 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC 252
Qy 61 GCGTACCCGCTTCGAGCAGCGGACATCGGCCAGCGGATGAGTGGCTCTTGTCTCCCGGGA 120
Db 251 GCGTACCCGCTTCGAGCAGCGGACATCGGCCAGCGGATGAGTGGCTCTTGTCTCCCGGGA 192
Qy 121 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTTAAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTTAAACGTGCGC 132

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QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGCGAGCGGAACCTTGTGGCGCGTGAAATTGT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
131 GAGGACTCCGGTATCGTCAAGGTTCCGTGCGAGCGGAACGTTGTGGCGCGTGAAATTGT 72
QY 241 ACCGGCCCGCGCGAATGTTCTGTGTGCATCACTTGTGTAGCCCTTCGGCTCGTCTCGG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
71 ACCGGCCCGCGCGAATGTTCTGTGTGCATCACTTGTGTAGCCCTTCGGCTCGTCTCGG 12
QY 301 TTTGTGCGACAT 311
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
11 TTTGTGCGACAT 1
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RESULT 10

US-10-647-089-52/c

; Sequence 52, Application US/10647089

; Publication No. US20040063923A1

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: STAN102CON the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/10/647,089

; CURRENT FILING DATE: 2003-08-21

; PRIOR APPLICATION NUMBER: US/09/894,844

; PRIOR FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-10-647-089-52

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Query Match 20.3%; Score 311; DB 7; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGTTTCAGCTCGGAACCTCGATCCCGAGGACCTGAAATCCCATGCGCGGAACCGACC 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
311 ATGTTTCAGCTCGGAACCTCGATCCCGAGGACCTGAAATCCCATGCGCGGAACCGACC 252
QY 61 GGTATCCCGCTTCCAGCAGCGGACATCGGCGAGCGTAGTGGCTCTTGTCCCGGGA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
251 GGTATCCCGCTTCCAGCAGCGGACATCGGCGAGCGTAGTGGCTCTTGTCCCGGGA 192
QY 121 AAGAGCGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCTAACGTCGCG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
191 AAGAGCGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCTAACGTCGCG 132
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGCGAGCGGAACGTTGTGGCGGTGAAATTGT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
131 GAGGACTCCGGTATCGTCAAGGTTCCGTGCGAGCGGAACGTTGTGGCGGTGAAATTGT 72
QY 241 ACCGGCCCGCGCGAATGTTCTGTGTGCATCACTTGTGTAGCCCTTCGGCTCGTCTCGG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
71 ACCGGCCCGCGCGAATGTTCTGTGTGCATCACTTGTGTAGCCCTTCGGCTCGTCTCGG 12
QY 301 TTTGTGCGACAT 311
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
11 TTTGTGCGACAT 1
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RESULT 11

US-10-282-122A-26084/c

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; Sequence 26084, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26084
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-26084
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Query Match 12.7%; Score 194.4; DB 7; Length 366;
Best Local Similarity 73.7%; Pred. No. 5.6e-43;
Matches 261; Conservative 0; Mismatches 91; Indels 2; Gaps 1;
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QY	943	CGGGATGGAAGCACACCGTCGTCCTT--GGGGTGCCTGCGAGGAATGCGACCTGTTTGT 1000
Db	354	CGGGGTGGAACACACACCGTGGTGGTGGGATCTCTCGTGCAGCCCGCCACTGTTTGT 295
QY	1001	TAGCTTACGCGATCGATCCAGTAGTCGTCGCCCTCGACAACGCGACGTACTCGCCGG 1060
Db	294	CAATTTCAACGGGTGACCCAGTAGTCGTCGCCCTCGCACAGCGGATGACTCGCCAG 235
QY	1061	AGCGGCCGACAGGGCGCGGTCAGGTTCCATTGAGGCCGAGGTTTTCGGTCTCGAAGAT 1120
Db	234	CGCGCGGACAGGGCACCGTGGTGGGTTGGCGTTGAGGCCGAGTTTCTCGACCGCAGGAT 175
QY	1121	CGCGCGGAACAGTGCGGGTACCGCTCGGCGTACTCACGCGATGATCGCGGGGTGCGCATC 1180
Db	174	GGGCCGGAAGAGTTCCGATGCGGCGTTCGCGGTATTCTCGATGATTTCGGGGTGTGCGCATC 115
QY	1181	GGTCCAGCGTCTCGGCGACGATGATCTCCACCGGGAAGTCGGTTTGTGTCGAGAA 1240
Db	114	GGTCCAGGCGATCGTCGGCGACTATTACCTCCATCGGAAAGTCTACCCGCTGGCGAGGAA 55
QY	1241	GCTGTGGAAGGCTGACGGCGGTAGCCCGCTGGTGTGAGTGGTTCGAGACGAT 1294

Db

54 GCCGTCCAA CGTGT CGCGGACATATGTTGCTGGTGTGGGTGGTTGACACCAT 1

RESULT 12

RESULT 12
US-10-282-122A-25902/c
; Sequence 25902, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

Query Match	6.8%	Score 104.8;	DB 7;	Length 276;
Best Local Similarity	75.6%	Pred. No. 1.7e-18;		
Matches 130;	Conservative	0;	Mismatches 42;	Indels 0;
				Gaps 0;

RESULT 13

US-10-282-122A-13587/c

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; Sequence 13587, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13587
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Burkholderia fungorum
US-10-282-122A-13587

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Query Match	4.7%;	Score 72.8;	DB 7;	Length 951;
Best Local Similarity	54.5%;	Pred. No. 1e-09;		
Matches 146;	Conservative 0;	Mismatches 122;	Indels 0;	Gaps 0;
QY	1026	TGTCGCCCTTCGCACAAACGGGACGTACTCGCCCGAGCGCCCGACAGGGCGCCGGTCA	GG	1085
Db	275	TGTCGCCCTTCGATGTTTCGCGATGAATTGCGCCCTTCGCGATCGCCACGGTATCGGCGAAA		216
QY	1086	TTCCCAATTGAGCCCGAGGTTTTTCGGTCTCTGAAGATCGGCCGGAAACAGTTCGGGGTACCCG		1145
Db	215	TTGCGTGCACGCCGACGTTGGTGTGCTGGCGAAACACCTTGATCAGGTCCGGGTAAACGC		156
QY	1146	TGCGCGTACTCAGCGATGATCGCCGGGTGGCATCGTTCGACCGCTGTCGGCGACGATG		1205
Db	155	GCCCGGAAGACTCGAATGACAGCCATGTAATTGTCGGGGGAATTGTATATCGCCACGATG		96
QY	1206	ATCTCCACCGGGAAGTCGGTTTTCGTCTCGAGAAAGCTGTCTGAAGCGCTTCACGGGGTAG		1265
Db	95	ATCTCGAATGGCACATCGAGATGCTGTCGACGACGCTTTGCAGACATGCACCCGACGTAC		36
QY	1266	CCGCGCTGTTGTGAGTGTTCGAGACGA		1293
Db	35	TCGTCTCTCCGGGTAAACAAAGCACGATGA		8

RESULT 14

US-10-282-122A-35893/c

; Sequence 35893, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangou

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35893

; LENGTH: 1395

; TYPE: DNA

; ORGANISM: Streptococcus mutans

US-10-282-122A-35893

Query Match 4.3%; Score 65.2; DB 7; Length 1395;
Best Local Similarity 50.0%; Pred. No. 1.2e-07;
Matches 163; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 978 TCAGGAATGCACCTGTTTGTAGCTTCAGCGGATCGATCGATGAGTCGTCGCGCTG 1037
DB 332 TCTAAAGATCAATTTGTTTGAAGCTTAAAGGTCATCAATAATCATCACCATCA 273

QY 1038 CACAACGCGACCTACTCGCGCGGACGCGGCGGTCAGGTCAGGTCACATGAGG 1097
DB 272 CATCTGCAATGACTGTCTCTAGCTTCTTACAAATATCGACCAAGTTTGTAAAT 213

QY 1098 CCGAGGTTTTCGGTCTGGAAGATCGCGCGGAACAGCTGCGGTAACGCTCGCGGTACTCA 1157
DB 212 CCTTGATTTCTTGTATTAAGAAAGCCGCAATTAATCTGGATCTGTTTTGTAGAGTT 153

QY 1158 CGGATGATCGCGGGTGCATCGGTCGACGCTCGCGGACGATGATCTCCACCGG 1217
DB 152 TTTATGATATGAATGAATGATGTTGTGAAGATCATCAACAAATATGATTTATATGA 93

QY 1218 AAGTCGGTTTGTGTCGAGAAAGCTGTCGAAGGCTGACGGGCGGTAGCCGCTGGTTG 1277
DB 92 AATGATGTTTCTGTTTCAGGAACATCAATAGCTTCAACATCCAGCTTCTTTATTA 33

QY 1278 TCAGTGTGCGACGATGCTACCTT 1303

DB 32 TAAATGGTCAAAATAATGGATACTTT 7

RESULT 15

US-09-976-059-1/c

; Sequence 1, Application US/09976059

; Patent No. US2002016474A1

; GENERAL INFORMATION:

; APPLICANT: Farnet, Chris

; APPLICANT: Zazopoulos, Emmanuel

; APPLICANT: Staffa, Alfredo

; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin

; FILE REFERENCE: 3019-PCT

; CURRENT APPLICATION NUMBER: US/09/976,059

; CURRENT FILING DATE: 2001-10-15

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 88421

; TYPE: DNA

; ORGANISM: Actinoplanes sp.

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2077)..(3078)

; OTHER INFORMATION: ORF 1; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (3118)..(4032)

; OTHER INFORMATION: ORF 2; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (4038)..(5048)

; OTHER INFORMATION: ORF 3; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (4038)..(5048)

; OTHER INFORMATION: ORF 3; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (6665)..(5814)

; OTHER INFORMATION: ORF 4; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (7703)..(6693)

; OTHER INFORMATION: ORF 5; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (9464)..(8130)

; OTHER INFORMATION: ORF 6; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (9691)..(10761)

; OTHER INFORMATION: ORF 7; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (12751)..(10829)

; OTHER INFORMATION: ORF 8; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (13617)..(12802)

; OTHER INFORMATION: ORF 9; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (15203)..(13614)

; OTHER INFORMATION: ORF 10; negative strandedness

; NAME/KEY: misc feature

; LOCATION: (15591)..(15863)

; OTHER INFORMATION: ORF 11; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (15880)..(19035)

; OTHER INFORMATION: ORF 12; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (19032)..(39713)

; OTHER INFORMATION: ORF 13; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (39713)..(65800)

; OTHER INFORMATION: ORF 14; positive strandedness

; NAME/KEY: misc feature

; LOCATION: (65826)..(66530)

; OTHER INFORMATION: ORF 15; positive strandedness


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; NAME/KEY: misc_feature
; LOCATION: (66546)..(67370)
; OTHER INFORMATION: ORF 16; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (67384)..(70059)
; OTHER INFORMATION: ORF 17; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (70099)..(70662)
; OTHER INFORMATION: ORF 18; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (70659)..(71906)
; OTHER INFORMATION: ORF 19; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (73439)..(71964)
; OTHER INFORMATION: ORF 20; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (74216)..(73563)
; OTHER INFORMATION: ORF 21; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (75424)..(74213)
; OTHER INFORMATION: ORF 22; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (75535)..(76464)
; OTHER INFORMATION: ORF 23; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (78110)..(76449)
; OTHER INFORMATION: ORF 24; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

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Query Match          3.7%; Score 57.4; DB 3; Length 88421;
Best Local Similarity 43.4%; Pred. No. 2.1e-05;
Matches 262; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

QY      673  GCCACATGCTTGGGCGTGCGCGGATACACGCCATGTTGTCGGGCAACATGGCGATGT 732
DB      40820  GCGCGAGGGCGGACCGCGCGCGGACCGCGGATGATGTTCTCCACGGCGACGG 40761

QY      733  CGCCATGCAACCGCGTCCGCGACGTGCGAGATACAGTCCAGGGGCATGACGTGCGCAGGAA 792
DB      40760  CCACCTGGAAACAGCGGTGGCGCTCAGCGACCGCGACGCGCGAGCTCTCTGACGAGCT 40701

QY      793  TGTCTGCTGATGCGCTCAGGCGGACGCTACACGCCCGAGTTGTTCTGGATGAAGTTTCATCA 852
DB      40700  TCTCGAACCGGACAGCTCTGTGGTCCGTACGCGTTCGAGGGCGCGCTCGCGGACCTGCGCGCA 40641

QY      853  AGATCAACGATCCAGGCTCAAGTTGCTCCCGCACCCCGAACCGGGGGGAACCTTCGAGTCTCT 912

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Search completed: February 20, 2006, 02:26:36
Job time : 1324.13 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 01:43:06 ; Search time 500.571 Seconds
(without alignments)
6500.886 Million cell updates/sec

Title: US-09-673-476-1_COPY_11200_12800

Perfect score: 1533

Sequence: 1 atgttcagctcgacacctc.....gtcgtgctgtgtgctgc 1533

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1533	100.0	12732	8	US-10-802-796-1
2	1119	73.0	1119	12	Sequence 1, Appli
3	311	20.3	894	12	Sequence 53, Appl
4	57.4	3.7	88421	12	Sequence 52, Appl
5	56	3.7	1236	12	Sequence 1, Appli
6	53	3.5	2155	12	Sequence 127, App
7	53	3.5	2937	9	Sequence 122, App
8	53	3.5	6200	8	Sequence 8, Appli
9	53	3.5	6200	8	Sequence 1, Appli
10	53	3.5	37500	8	Sequence 1, Appli
11	49.6	3.2	1386	8	Sequence 133, App
12	47.2	3.1	10968	12	Sequence 35, Appl
13	47.2	3.1	78869	12	Sequence 11, Appli
14	45.4	3.0	1356	12	Sequence 78, Appl
15	45	2.9	5679	12	Sequence 36, Appl
16	44.8	2.9	897	8	Sequence 3, Appli
17	44.8	2.9	3624	7	Sequence 6, Appli
18	44.8	2.9	8651	8	Sequence 48, Appl
19	44.6	2.9	5301	12	Sequence 40, Appl
20	43.8	2.9	607	6	Sequence 762706,

C 21	43.8	2.9	607	6	US-09-925-065A-830710	Sequence 830710,
C 22	43.8	2.9	614	6	US-09-925-065A-770571	Sequence 770571,
C 23	43.8	2.9	614	6	US-09-925-065A-835176	Sequence 835176,
C 24	43.4	2.8	607	6	US-09-925-065A-762705	Sequence 762705,
C 25	43.4	2.8	614	6	US-09-925-065A-770570	Sequence 770570,
C 26	42.8	2.8	4509	12	US-11-087-100-5	Sequence 5, Appli
C 27	42.8	2.8	4509	12	US-11-087-084-5	Sequence 5, Appli
C 28	42.8	2.8	4509	12	US-11-087-085-5	Sequence 2, Appli
C 29	42.6	2.8	37507	8	US-10-522-037-2	Sequence 319, App
C 30	42.2	2.8	5121	8	US-10-775-169-319	Sequence 48, Appl
C 31	42	2.7	1119	8	US-10-858-730-48	Sequence 15, Appl
C 32	41.6	2.7	912	8	US-10-432-483-15	Sequence 48, Appl
C 33	41.6	2.7	8651	8	US-10-432-483-48	Sequence 2, Appli
C 34	41.2	2.7	14172	12	US-11-075-185-2	Sequence 177, App
C 35	41	2.7	1629	8	US-10-858-730-177	Sequence 115, App
C 36	40.8	2.7	990	7	US-10-714-887-115	Sequence 20, Appl
C 37	40.8	2.7	2302	12	US-11-110-082-20	Sequence 7, Appli
C 38	40.6	2.6	546	12	US-11-089-945-4	Sequence 1, Appli
C 39	40.6	2.6	4551	8	US-10-220-824-7	Sequence 7054, Ap
C 40	40.6	2.6	88421	12	US-11-205-109-1	Sequence 2958, Ap
C 41	40.4	2.6	1400	12	US-11-136-527-7054	Sequence 142, App
C 42	40.4	2.6	2186	12	US-11-136-527-2958	Sequence 18, Appl
C 43	40.4	2.6	3513	8	US-10-858-730-142	Sequence 34, Appl
C 44	40.2	2.6	978	12	US-11-143-980-18	
C 45	40.2	2.6	11070	12	US-11-075-185-34	

ALIGNMENTS

RESULT 1

US-10-802-796-1
; Sequence 1, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-1

Query Match	100.0%;	Score 1533;	DB 8;	Length 12732;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1533;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGTTTCAGTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC	60	
Db	11200	ATGTTTCAGTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGAACCCGACC	11259	
Qy	61	GGGTACCCGCTTCCAGGACCGGACATCGCGAGCGTAGTGGCTCTTGTCCCGGGA	120	
Db	11260	GGGTACCCGCTTCCAGGACCGGACATCGCGAGCGTAGTGGCTCTTGTCCCGGGA	11319	
Qy	121	AAGACGGTTTCCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTTCTTAACGTGCGC	180	

Db 11320 AGACGGTTTCAGATCCCGCGCGGAGATGACACGAGCATTCGTCATACGTCGC 11379
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCGAGCGAACGTTGCGCGGTGAATTGT 240
Db 11380 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCGAGCGAACGTTGCGCGGTGAATTGT 11439
QY 241 ACCGCGCGCGCGAATGTTCTGTGTCATCATCTGTTAGCCCTTCGGCTGTCCTGGG 300
Db 11440 ACCGCGCGCGCGAATGTTCTGTGTCATCATCTGTTAGCCCTTCGGCTGTCCTGGG 11499
QY 301 TTTGTGCAATGTCAGGTCGACAGCCGCTCGAGCCGAGGAGGSCACACATCCACGA 360
Db 11500 TTTGTGCAATGTCAGGTCGACAGCCGCTCGAGCCGAGGAGGSCACACATCCACGA 11559
QY 361 GCGCCCTCGGGTCGCGCTCGCGCGCGGAGCTTCGCCCACTGGGTCTTTGAGCGCGCG 420
Db 11560 GCGCCCTCGGGTCGCGCTCGCGCGCGGAGCTTCGCCCACTGGGTCTTTGAGCGCGCG 11619
QY 421 CGGGTGTGCGCGCGGGTCTGAGCGCGCAGCATGCGGATCGGGATCGCGCGGATCG 480
Db 11620 CGGGTGTGCGCGCGGGTCTGAGCGCGCAGCATGCGGATCGGGATCGCGCGGATCG 11679
QY 481 TTTCTGTCAGCGCGCGCCCTCGCGGCTGGAACGTTGGCGATCTCGCGAAGGATCC 540
Db 11680 TTTCTGTCAGCGCGCGCCCTCGCGGCTGGAACGTTGGCGATCTCGCGAAGGATCC 11739
QY 541 AGTCGCGCATGACGGCGATGAGCTCTCGCGCGCGGGTCTCCCGGAAACAGGTCGAGCA 600
Db 11740 AGTCGCGCATGACGGCGATGAGCTCTCGCGCGCGGGTCTCCCGGAAACAGGTCGAGCA 11799
QY 601 TCGGCTCAACAGTCGCGCGATGCGCGCGGACCTGCTCAACAGAACTTTGGGGTCCA 660
Db 11800 TCGGCTCAACAGTCGCGCGATGCGCGCGGACCTGCTCAACAGAACTTTGGCGGTCCA 11859
QY 661 CCACCTGGTTGTGCCACATGCTTGGGCTGCGCGGATACAGGCGCATGTTGGGCA 720
Db 11860 CCACCTGGTTGTGCCACATGCTTGGGCTGCGCGGATACAGGCGCATGTTGGGCA 11919
QY 721 ACATGCGCATGTCGCAATCACCGGTGCGGACGTCGAGATACCACTCAGGGGCA 780
Db 11920 ACATGCGCATGTCGCAATCACCGGTGCGGACGTCGAGATACCACTCAGGGGCA 11979
QY 781 CGTCGCGAGATGTCGTGAGCGTCGAGCGGACGTTACAGCGCGAGTTGTTGTCGA 840
Db 11980 CGTCGCGAGATGTCGTGAGCGTCGAGCGGACGTTACAGCGCGAGTTGTTGTCGA 12039
QY 841 TGAAGTTTCATCAAGATCAACGATCCAGGCTCAAGTTGCCCGCACCCGAAACCGGGGGA 900
Db 12040 TGAAGTTTCATCAAGATCAACGATCCAGGCTCAAGTTGCCCGCACCCGAAACCGGGGGA 12099
QY 901 ACTTCGAGTCTTGGCATGCGGCTCTCCCATATCACTCGGACGGGATGGAAGCACACG 960
Db 12100 ACTTCGAGTCTTGGCATGCGGCTCTCCCATATCACTCGGACGGGATGGAAGCACACG 12159
QY 961 TCGTCTTGGGTCGCGGTGAGGAATGCGACTGTTTGTCTTACGTCAGCGATCGATCC 1020
Db 12160 TCGTCTTGGGTCGCGGTGAGGAATGCGACTGTTTGTCTTACGTCAGCGATCGATCC 12219
QY 1021 AGTAGTCTGTCGCTCGCAACGAGACGTAAGTTGCGCGAGCGCGGACAGGCGCGCG 1080
Db 12220 AGTAGTCTGTCGCTCGCAACGAGACGTAAGTTGCGCGAGCGCGGACAGGCGCGCG 12279
QY 1081 TCAGGTTCCATTGAGCGCGAGGTTTTCGGTCTCTGAAGATCGCGCGGAAACAGTGGCGGT 1140
Db 12280 TCAGGTTCCATTGAGCGCGAGGTTTTCGGTCTCTGAAGATCGCGCGGAAACAGTGGCGGT 12339
QY 1141 ACCGCTCGCGGTACTCACGGATGATCGCGGGGTGCGATCGGTTCGACGCGGTGTCGGCGCA 1200
Db 12340 ACCGCTCGCGGTACTCACGGATGATCGCGGGGTGCGATCGGTTCGACGCGGTGTCGGCGCA 12399
QY 1201 CGATGATCTCCACCGGGAAGTCGGTTGCTGTCGAGAAAGCTGTGGAAGGCTTCGAGGCGCTTCACGCG 1260

Db 12400 CGATGATCTCCACCGGGAAGTCGGTTTGTGTCGAGAAAGCTGTGCAAGGCTTGACGGG 12459
QY 1261 CQTAGCCCGCTGGTTGTGAGTTCGAGACGATGCTCACTTGGGGCAAAAGCTGGGGAC 1320
Db 12460 CQTAGCCCGCTGGTTGTGAGTTCGAGACGATGCTCACTTGGGGCAAAAGCTGGGGAC 12519
QY 1321 TCACGCTCGGCGCTTTTCTGCGCGCGCCGAAAGGTTATTCGATGCGGAAACGTAATCGC 1380
Db 12520 TCACGCTCGGCGCTTTTCTGCGCGCGCCGAAAGGTTATTCGATGCGGAAACGTAATCGC 12579
QY 1381 CTGTGCGCCCGCGCGCTGCGCGCTGCGTGGTTCGCGGACCTACCGGACACGCT 1440
Db 12580 CTGTGCGCCCGCGCGCTGCGCGCTGCGTGGTTCGCGGACCTACCGGACACGCT 12639
QY 1441 GCGGAAGTATAGCGAGGTCACCTGACGTTGGGTCGAAACCGCGTGGCGCGGTTGGG 1500
Db 12640 GCGGAAGTATAGCGAGGTCACCTGACGTTGGGTCGAAACCGCGTGGCGCGGTTGGG 12699
QY 1501 GCGACGCTCTCGAGTCGGTCTGCTGGTGGCTCGC 1533
Db 12700 GCGACGCTCTCGAGTCGGTCTGCTGGTGGCTCGC 12732

RESULT 2
US-11-143-401-53/c
; Sequence 53, Application US/11143401
; Publication NO. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-53

Query Match 73.0%; Score 1119; DB 12; Length 1119;
Best Local Similarity 100.0%; Pred. No. 3.7e-278; Mismatches 0; Indels 0; Gaps 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 GGCTCGACAGCGCGCTCGGAGCGGGAGGGCCACACATCCAGAGCCCTTCGGGCTCGG 376
Db 1119 GGCTCGACAGCGCGCTCGGAGCGGGAGGGCCACACATCCAGAGCCCTTCGGGCTCGG 1060
QY 377 CQTGCGCGCGGAGCTTCGCGCACCTGGGTCTTTGAGCGCGCGCGGGTGTGCGCCCGCG 436
Db 1059 CQTGCGCGCGGAGCTTCGCGCACCTGGGTCTTTGAGCGCGCGCGGGTGTGCGCCCGCG 1000
QY 437 GTGCTGCAAGCGCCAGCATGGCGATCCGGGATGGCGCGATGTTCTTCGAGCGCGCG 496
Db 999 GTGCTGCAAGCGCCAGCATGGCGATCCGGGATGGCGCGATGTTCTTCGAGCGCGCG 940
QY 497 GCGCCCTCTCGGGCTTGGAAACGTTGGCGATCTGGGGAGGATCCAGTCCGGCCATGACGCG 556
Db 939 GCGCCCTCTCGGGCTTGGAAACGTTGGCGATCTGGGGAGGATCCAGTCCGGCCATGACGCG 880

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QY 557 GATGAGCTCTCGCGCGCGGGTCTCCCGGAAACAGGTGAGCATCGCGTCAAAACGTGCG 616
Db 879 GATGAGCTCTCGCGCGCGGGTCTCCCGGAAACAGGTGAGCATCGCGTCAAAACGTGCG 820
QY 617 CGATGCCCCGGACCTCGCTCAACAGAACTTTGGCGGGTCCACCACTGGTGTGGCCA 676
Db 819 CGATGCCCCGGACCTCGCTCAACAGAACTTTGGCGGGTCCACCACTGGTGTGGCCA 760
QY 677 CATGSCCTTGGGCGGTGGCGCGATACACGGCGCATGGTGTCCGGGCAACATGCGCATGTCGCC 736
Db 759 CATGSCCTTGGGCGGTGGCGCGATACACGGCGCATGGTGTCCGGGCAACATGCGCATGTCGCC 700
QY 737 ATGACCGCGTCCGAGACGTGACAGATACAGTCAAGGGGATGACGTGCGCAGGAATGTC 796
Db 699 ATGACCGCGTCCGAGACGTGACAGATACAGTCAAGGGGATGACGTGCGCAGGAATGTC 640
QY 797 GTGCTAGCGCTCCAGCGGACGGGTACACGGCGAGTGGTCTGATGAAGTTTCATCAAGAT 856
Db 639 GTGCTAGCGCTCCAGCGGACGGGTACACGGCGAGTGGTCTGATGAAGTTTCATCAAGAT 580
QY 857 CAACGATCCAGGCTCAAGTTGGCCCGCACCCGAAACCGGGGGAACTTCAGTCCCTTGGC 916
Db 579 CAACGATCCAGGCTCAAGTTGGCCCGCACCCGAAACCGGGGGAACTTCAGTCCCTTGGC 520
QY 917 ATGGCGCTCTCCCATATCACTCGGACGGGATGGAAGCAACCGTCTGTGGGGTGGCG 976
Db 519 ATGGCGCTCTCCCATATCACTCGGACGGGATGGAAGCAACCGTCTGTGGGGTGGCG 460
QY 977 GTGAGGAATGCACTGTTGCTTAGCTTACGGGATCGATCCAGTAGTCTGTCGCGCTC 1036
Db 459 GTGAGGAATGCACTGTTGCTTAGCTTACGGGATCGATCCAGTAGTCTGTCGCGCTC 400
QY 1037 GCACAAACGCGACCTACTCGCGCGAGCGCGCGACAGGGCGCGGTTCAGGTTCCCATTTAG 1096
Db 399 GCACAAACGCGACCTACTCGCGCGAGCGCGCGACAGGGCGCGGTTCAGGTTCCCATTTAG 340
QY 1097 GCCGAGTTTTCGGCTCTGAAGATCGCGCGAAACAGTGGGGTACCGTTCGCGCTACTC 1156
Db 339 GCCGAGTTTTCGGCTCTGAAGATCGCGCGAAACAGTGGGGTACCGTTCGCGCTACTC 280
QY 1157 ACGGATGATCGCGCGGGTGGCATCGGTGACCGGTGTGGCGACATGATCTCCACGG 1216
Db 279 ACGGATGATCGCGCGGGTGGCATCGGTGACCGGTGTGGCGACATGATCTCCACGG 220
QY 1217 GAAGTCGGTTTTGCTGCTCGAGAAAGTGTGCGAGGCTGACGGCGGTAGCGCGCTGGTT 1276
Db 219 GAAGTCGGTTTTGCTGCTCGAGAAAGTGTGCGAGGCTGACGGCGGTAGCGCGCTGGTT 160
QY 1277 GTGAGTGTGCGACGATGCTACCTTTGGGCGAAAGCTGGGGACTCACCGTTCGCGCCTTT 1336
Db 159 GTGAGTGTGCGACGATGCTACCTTTGGGCGAAAGCTGGGGACTCACCGTTCGCGCCTTT 100
QY 1337 TCCTGCGCGCGCGAAGGTTATTCGATGCGGAAAGTGAATGCTGTCGCGCGCGCGCG 1396
Db 99 TCCTGCGCGCGCGAAGGTTATTCGATGCGGAAAGTGAATGCTGTCGCGCGCGCGCG 40
QY 1397 TCGGCGCTGCTGCGCTGCTGCTGCGCGGACGTACGGCAC 1435
Db 39 TCGGCGCTGCTGCGCTGCTGCTGCGCGGACGTACGGCAC 1
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RESULT 3

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US-11-143-401-52/c
; Sequence 52, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
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; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
; US-11-143-401-52
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Query Match 20.3%; Score 311; DB 12; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.5e-70;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 311 ATGTTTCAGTCCGAAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGCAACCCGACC 252
QY 61 GCGTACCCGCTTCCAAAGCAGCGGACATCGGCCAGCGTAGGTGGTCTTTGTCCCGGGA 120
Db 251 GCGTACCCGCTTCCAAAGCAGCGGACATCGGCCAGCGTAGGTGGTCTTTGTCCCGGGA 192
QY 121 AAGACGGTTTCCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTCTAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTCTAACGTGCGC 132
QY 181 GAGGACTCGGTATTCGTCAAGTTCGTGTCGAGCGAAACGTTGTGGCGGCGTGAATTGT 240
Db 131 GAGGACTCGGTATTCGTCAAGTTCGTGTCGAGCGAAACGTTGTGGCGGCGTGAATTGT 72
QY 241 ACCGCGCGCGCGAAATGTTCTGTGCGCATCATCTGTTAGCCCTTCGGCTGCTCTGGG 300
Db 71 ACCGCGCGCGCGAAATGTTCTGTGCGCATCATCTGTTAGCCCTTCGGCTGCTCTGGG 12
QY 301 TTTGTCGACAT 311
Db 11 TTTGTCGACAT 1
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RESULT 4

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US-11-205-109-1/c
; Sequence 1, Application US/11205109
; Publication No. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
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, NAME/KEY: misc feature
, LOCATION: (3118)..(4032)
, OTHER INFORMATION: ORF 2; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (4038)..(5048)
, OTHER INFORMATION: ORF 3; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (6665)..(5814)
, OTHER INFORMATION: ORF 4; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (7703)..(6693)
, OTHER INFORMATION: ORF 5; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (9464)..(8130)
, OTHER INFORMATION: ORF 6; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (9691)..(10761)
, OTHER INFORMATION: ORF 7; positive strandedness
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, NAME/KEY: misc feature
, LOCATION: (12751)..(10829)
, OTHER INFORMATION: ORF 8; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
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, OTHER INFORMATION: ORF 9; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (15203)..(13614)
, OTHER INFORMATION: ORF 10; negative strandedness
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, NAME/KEY: misc feature
, LOCATION: (15591)..(15863)
, OTHER INFORMATION: ORF 11; positive strandedness
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, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (19032)..(39713)
, OTHER INFORMATION: ORF 13; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (39713)..(65800)
, OTHER INFORMATION: ORF 14; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (65826)..(68530)
, OTHER INFORMATION: ORF 15; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (66546)..(67370)
, OTHER INFORMATION: ORF 16; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (67384)..(70059)
, OTHER INFORMATION: ORF 17; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (70059)..(70662)
, OTHER INFORMATION: ORF 18; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (70659)..(71906)
, OTHER INFORMATION: ORF 19; positive strandedness
, FEATURE:
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, NAME/KEY: misc feature
, LOCATION: (73439)..(71964)
, OTHER INFORMATION: ORF 20; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (74216)..(73563)
, OTHER INFORMATION: ORF 21; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (75424)..(74213)
, OTHER INFORMATION: ORF 22; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (75535)..(76464)
, OTHER INFORMATION: ORF 23; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (78110)..(76449)
, OTHER INFORMATION: ORF 24; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (79864)..(78107)
, OTHER INFORMATION: ORF 25; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (81624)..(79861)
, OTHER INFORMATION: ORF 26; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (81909)..(81682)
, OTHER INFORMATION: ORF 27; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (82346)..(82062)
, OTHER INFORMATION: ORF 28; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (82587)..(84446)
, OTHER INFORMATION: ORF 29; positive strandedness
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, LOCATION: (84481)..(85548)
, OTHER INFORMATION: ORF 30; positive strandedness
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, LOCATION: (85556)..(86845)
, OTHER INFORMATION: ORF 31; positive strandedness
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, NAME/KEY: misc feature
, LOCATION: (87372)..(86803)
, OTHER INFORMATION: ORF 32; negative strandedness
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, NAME/KEY: misc feature
, LOCATION: (87494)..(88420)
, OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
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US-11-205-109-1
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Query Match      3.7%; Score 57.4; DB 12; Length 88421;
Best Local Similarity 43.4%; Pred. No. 2.6e-05;
Matches 262; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

QY 673 GGCACATGCTTTGGCGTGGCGGATACACGGCCATGTTGTTCGGGCACATGGCGATGT 732
    |||||
DB 40820 GCCCGAGGGCGGGACCGCGCGCGCATCAGGTCTCCACGGCAGCG 40761

QY 733 CGCCATGCACCGGTGCGGAGTGCAGATACAGTCCAGGGGCGATGCTCGGAGGAA 792
    |||||
DB 40760 CCACCTGGAACAGCGGTGCGGCTCAGCAGCCGACGCGGAGCTCTCTCAGAGCT 40701

QY 793 TGTGCTGCTAGCGCTCGAGGCGACGGTACACGGCCGAGTTGGTCTCGATGAAGTTCA 852
    |||||
DB 40700 TCTCGAAGCGGACGCTCTGTTGGCCGTACGCGTGGAGGGCCCGCTCGCGGACCTCGCGCA 40641
```

QY 853 AGATCAACGCGATCCAGGCTCAAGTTGCCCGCCAGCCCGGGGGAACCTTCAGATCCT 912
Db 40640 GCAGGTCGCGAAGGTCCGGTCCCGGTCAAGTCCGGCCCGGATCACCAAGTTGTTGAAGA 40581
QY 913 TGGCATGCGCGTCTCCATATACATCCGAGCGGATGGAAGACACCGTCTGTTGGGGT 972
Db 40580 AGCAGCGGACGAGGTCTGTCAGGCGCGGTGCGTGGCGCGGCGCACACCGTCCGATCG 40521
QY 973 GCGGTCCAGGAAATGCGACCTGTTTGTAGCTTCAGCGGATCGATCCAGTAGTCTGTCGG 1032
Db 40520 GCAGGTCGTCGCCCGCCAGCCCGAAGACCATGGCGGTGCGCGGTGACGCGCA 40461
QY 1033 CTTGCGCAACGCGACGTACTCGCGAGCGCGCGACAGGCGCGCGTTCAGGTTCCCAT 1092
Db 40460 TGAAGAGCGTGGCGCGAGCTCGCGGTGAGGCGGTTCAGTCCGCGTGGCGCGCG 40401
QY 1093 TGAGGCGGAGTTTTCGTTCTGAAGATCGCGCGGAACACGTGGGGTACCGTCCGCGT 1152
Db 40400 GCACGCGGAATCGGCGCATGTGCGCGCGGACGACGACGCGGCGCGCGTGGTTCGG 40341
QY 1153 ACTCAGCGATGATCGCGCGGTGCGATCGGTTCGACGCGGTCTGCGGCGACGATCTCCA 1212
Db 40340 CCGCAGCGCGAGCTCTCGGGGCTCCCGCGAGCGCGGACCGCCAAATAGCCAGCTGCT 40281
QY 1213 CCGGGAAGTCGTTTGTCTGTCGAGAAAGTGTGGAAGGCTGACGCGGCGTAGCCCGCT 1272
Db 40280 CGCGCAGGAGCTCTCGGCTGTCACCGCGCGCGGACCTCTCTGTCGACAGCGGT 40221
QY 1273 GGT 1275
Db 40220 AGT 40218

RESULT 5

US-11-143-401-127/c
; Sequence 127, Application US/11143401
; Publication No. US2006002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; PRIOR FILING DATE: 2005-06-01
; PRIOR FILING DATE: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-127

Query Match 3.7%; Score 56; DB 12; Length 1236;
Best Local Similarity 63.2%; Pred. No. 5.1e-05;
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1348 CGCAAGGTTATTCGATGGGACGTCGATCGCTGTGCGCGCGCGCGTCCGCGCTGCT 1407
Db 1062 CGGTGGGTTGATAGTCGCGCGCTCGATCGGTGCTTACGAGGCTACCCAGAACCGC 1003
QY 1408 GGCCTGTGTGCGCGGACCTAGCGACAGCTGGCGAGTATAGCGAGGTGCACTGAC 1467

Db 1002 GGCCTTGTGTGCGCGGAGCTGCGAGCAAGCTTCGCGAAACAGAGCGACGCAACATTTGGC 943
QY 1468 GTTGGGCTCGAACCGC 1483
Db 942 GTTGTCTCTGGAACGC 927

RESULT 6

US-11-122-329-122/c
; Sequence 122, Application US/11122329
; Publication No. US2006001927A1
; GENERAL INFORMATION:
; APPLICANT: Geraci, Mark
; APPLICANT: Bull, Todd
; APPLICANT: Voelkel, Norbert
; APPLICANT: Coldren, Chris
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
; FILE REFERENCE: 2848-54
; CURRENT APPLICATION NUMBER: US/11/122,329
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/568,129
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-122-329-122

Query Match 3.5%; Score 53; DB 12; Length 2155;
Best Local Similarity 48.0%; Pred. No. 0.0003;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
QY 319 CTCGACAGCCGCTCGAGCCGCGGAGGCGCACATCCACGACCCCTCGCGCTCGGC- 377
Db 1588 CTGCTCTGCGGTGGGAAGACGCGCGCGCCAGGCGCGCCACTCTGCGGTGCGGCTGCA 1529
QY 378 -GTGCGCGCGGAGCTTGGGCACTGGGTCTTTAGCGCGCGCGCGCGGTGTCGCCCGCG 436
Db 1528 GAGCCCGTTGTCCAGGTAGCGGTGACGTAGACAGCGCGCGCGCGCGCGCGCGCG 1469
QY 437 GTGCTGACGCGCGCATGCGGATCGCGGATGCGCGGATGCTTCTGACGCGCGCG 496
Db 1468 CAGCCCGAGGTACCGCGAGCTGCGGTGGGTGGGCGCGCGGTGCTGCTCGGTGCGTA 1409
QY 497 GCGCCCTCTCGGCGCTTGAACGTTGGCGATCTGGCGAAGGATCCAGTCGCGCATGACGGC 556
Db 1408 GATCAGCAGCGCGCGCGCGCGCTGCGCGCGCGCTGCGCGCGCTGCGCGCGCGCG 1349
QY 557 GATGAGCTCTGCGCGCGCGGTCTCCCGGGAACAGTGTGAGATCGCTCAAAACGTCGC 616
Db 1348 GAGCGCCACCGTGTGTTGTGTCTGTCAGGACGCTCCGCGCTGCGACACTTCGCGCC 1289
QY 617 CGCATGCCCGGACCTCGGTCAACAGAACTTTGCGGCTCCACCACTGTTGTGCCA 676
Db 1288 CTGCTCTCATCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1229
QY 677 CATGCTTGGGCGTGGCGG 695
Db 1228 CTGACGTCGCGCGCGCGG 1210

RESULT 7

US-11-202-566-8/c
; Sequence 8, Application US/11202566
; Publication No. US20060029609A1
; GENERAL INFORMATION:
; APPLICANT: Zankel et al.
; TITLE OF INVENTION: USE OF THE CHAPERONE RECEPTOR-ASSOCIATED PROTEIN (RAP) FOR THE
; FILE REFERENCE: 30610/39383

```
; CURRENT APPLICATION NUMBER: US/11/202,566
; CURRENT FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: US/10/600,862
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: RAP-IDU fusion sequence
US-11-202-566-8

Query Match      3.5%; Score 53; DB 9; Length 2937;
Best Local Similarity 48.0%; Pred. No. 0.00031;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGCTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 2469 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCGCTCGGGGTGCA 2410
QY 378 -GTCGCGCGCGGAGCTTCGCGCACTTGGGTCTTTGAGCCCGCGCGGTGTGCGCCCGCG 436
DB 2409 GAGCCCGTGTCCAGGTAGCGGTGACGTAGACAGGCCCGCGCGCGGGGACACCCCGG 2350
QY 437 GTGCTGACGCCAGCATCGCGGATCGGGGATGGCGCGGATGTTTCTCGAGCGCGGC 496
DB 2349 CAGCCGCAAGGTCACCGCAGCTCGCGTGGGTGGGCGCGGTGTCTGCTCGCGTA 2290
QY 497 GCGCCCTTCGCGGCTTGGACCTTGGCGATCTGGCGAAGATCCAGTCGGCCATGACGCG 556
DB 2289 GATCAGCACCGCGCGCGCGCAGCGCTCGCGCGGCGCTCGCGCGGTGGCGCTGGCCAG 2230
QY 557 GATGAGCTCTCTCGCGCGCGGCTCTCCCGGGAACAGGTCCAGCATCGCGTCAAACTCGC 616
DB 2229 GAGGCCACCGTGTGTTCTGTCCAGGACGCTCCGGCTCGGACACTTCGGCCAGAG 2170
QY 617 CGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCA 676
DB 2169 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGCGCGGTGAGCAGCGCTTGGCAACAG 2110
QY 677 CATGCTTTGGCGTGGCGG 695
DB 2109 CTGCACGTGCGCGGCGG 2091

RESULT 8
US-10-895-011-1/c
; Sequence 1, Application US/10895011
; Publication No. US20050281804A1
; GENERAL INFORMATION:
; APPLICANT: KAKKIS, EMIL D.
; TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
; FILE REFERENCE: 00800051CNUS01
; CURRENT APPLICATION NUMBER: US/10/895,011
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US/09/993,241
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1558)...(3510)
US-11-038-372-1

Query Match      3.5%; Score 53; DB 12; Length 6200;
Best Local Similarity 48.0%; Pred. No. 0.00032;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGCTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 3051 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCGCTCGGGGTGCA 2992
QY 378 -GTCGCGCGCGGAGCTTCGCGCACTTGGGTCTTTGAGCCCGCGCGGTGTGCGCCCGCG 436
DB 2991 GAGCCCGTGTCCAGGTAGCGGTGACGTAGACAGGCCCGCGCGGGGACACCCCGG 2932
QY 437 GTGCTGACGCCAGCATCGCGGATCGGGGATGGCGCGGATGTTTCTCGAGCGCGGC 496
DB 2931 CAGCCGCAAGGTCACCGCAGCTCGCGTGGGTGGGCGCGGTGTCTGCTCGCGTA 2872
QY 497 GCGCCCTTCGCGGCTTGGAACTTGGCGATCTGGCGAAGATCCAGTCGGCCATGACGCG 556
DB 2871 GATCAGCACCGCGCGCGCGCAGCGCTCGCGCGGCGCTGGGGCGGTGGCGCTGGCCAG 2812
QY 557 GATGAGCTCTCTCGCGCGCGGCTCTCCCGGGAACAGGTCCAGCATCGCGTCAAACTCGC 616
DB 2811 GAGGCCACCGTGTGTTCTGTCCAGGACGCTCCGGCTCGGACACTTCGGCCAGAG 2752
QY 617 CGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCA 676
DB 2751 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGCGCGGTGAGCAGCGGCTTGGCAACAG 2692
QY 677 CATGCTTTGGCGTGGCGG 695
DB 2691 CTGCACGTGCGCGGCGG 2673

RESULT 9
US-11-038-372-1/c
; Sequence 1, Application US/11038372
; Publication No. US20050260185A1
; GENERAL INFORMATION:
; APPLICANT: KAKKIS, EMIL D.
; TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
; FILE REFERENCE: 00800051CNUS01
; CURRENT APPLICATION NUMBER: US/11/038,372
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/895,011
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US/09/993,241
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 09/711,205
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/439,923
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1558)...(3510)
US-11-038-372-1

Query Match      3.5%; Score 53; DB 12; Length 6200;
Best Local Similarity 48.0%; Pred. No. 0.00032;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGCTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 3051 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCGCTCGGGGTGCA 2992
```


QY 378 -GTCCGGCGCGGAGCTTGGCCACTTGGGTCTTGGAGCCGCGCGGGGTGTCCGCCCGCG 436
Db 2991 GAGCCCGTTTCCAGGTAGCGGTAGAGTACAGCCCGCGCGGCGGACCCCGCG 2932
QY 437 GTCTCGAGCGCAGCATGCGGATCGGGATCGCGCGGATGTTCTCGAGCGCGGC 496
Db 2931 CAGCCCGAGGGTCAACCGCAGCTGGCGTTGGGTTGGGCGCGGGTGTCTGTCGTCGCGTA 2872
QY 497 GCGCCCTCCGGCGCTGGAGCTTGGCATCTGGCGAAGGATCCAGTCTGGCCCATGACGC 556
Db 2871 GATCAGGACCGCGCGCCAGCGCTCGCGCGGCCCTTGGGCGGTGGCGCTGGCCAG 2812
QY 557 GATGAGCTCTCCGCGCGCGGGTCTCCCGGGAACAGGTCTGAGCATCGCGTCAAACTCGC 616
Db 2811 GACGCCACCGTGTGTTGTTGTCAGGACGGTCCCGGCTCGACACTTCGSCCCAGAG 2752
QY 617 CGCATGCCCGGACCTCGGTGAACAGAACTTTGGCGGGTCCACACCTGTTGTGCCA 676
Db 2751 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGGCGGTGAGCACCGGCTTGGCAACAG 2692
QY 677 CATGCTTGGCGTGGCG 695
Db 2691 CTCACGTGCGCGGCGG 2673

RESULT 10

US-10-522-037-1

; Sequence 1, Application US/10522037

; Publication No. US20050282166A1

; GENERAL INFORMATION:

; APPLICANT: LIBRAGEN

; TITLE OF INVENTION: Method for the expression of unknown environmental DNA into adapt

; FILE OF INVENTION: B0149W0

; CURRENT APPLICATION NUMBER: US/10/522,037

; CURRENT FILING DATE: 2005-01-24

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 37500

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: DNA sequence of clone FS3-124.

US-10-522-037-1

Query Match 3.5%; Score 53; DB 8; Length 37500;

Best Local Similarity 46.5%; Pred. No. 0.00034;

Matches 259; Conservative 0; Mismatches 280; Indels 18; Gaps 2;

QY 672 TGCACATGCTTGGCGGTGGCGGATACACGGCCATGGTTCGGGCAACATGGCGATG 731
Db 17958 TTCGACATGTTGGTGTGTCGACGCTGTATGCGTCAGGGGTTCCGGGATGAACCGACC 18017
QY 732 TCGCCATGACCCGCTGCGGAGCTGCAGATACAGTCCAGGGGATGACGTCCGGCAGGA 791
Db 18018 GGGCCCTTCGCCAGAGGCGCAGCAGAGTCCAGTCTCTGACGCGGTGGATCCGGTTC 18077
QY 792 ATGTCTGTCGAGCGCTCGAGGCGACGTTACACGCGCGAGTTGGTCTGGATGAAGTTTCATC 851
Db 18078 GCGAACATCTCTGCGGAGCAGCGCGGCTTTGACCATGACCGAACGCGGTACGCGG 18137
QY 852 AAGATCAACGCATCCAGGTCAAGTTGCCCGCGCACCGGACCGGGGGGAATCTCGAGTCC 911
Db 18138 TTTTCGAGGACGAGGTTCGGGAGACAGCGCCCTTCGAGCGCGGCGGAAGATCGAGCGTGC 18197
QY 912 TTGGCATGGCGCTCTCCCATATCACTTCGAGCGGGATGGAAGCACACCGCTGCTTGGGG 971
Db 18198 AGACCTTCGCGCGCTCTGTCGATGAGCGCGCGCCGTATGATGAAGTCCAGTCCGGG 18257
QY 972 TGCCTGTCAGGGAATCGACCTGTTTGTCTTGTAGTTCAGCGGATTCGATTCAGTAGTCTCC 1031
Db 18258 TGCTGTCGGAAGAGATCGACCTGCGCGGGAATCTTTGGCGGATC---CCACGAGTCTGTCG 18314

QY 1032 GCCTCGCACACGCGACGTACTCGCGCGAGCGGCGCAGCGCGCGCGTTCAGGTTCCCA 1091
Db 18315 GGTTCAGCAGCGCCACGAAATTCCTCCCTCGCGCGCGCGCATGGCGGCGCG 18374
QY 1092 TTGAGCGCGAGGTTTTCGTCCTGAAGATCGCGCGGAAACAGTTCGCGGTACCGCTCGGG 1151
Db 18375 GCAAGCGCCGCTTGGC-----CTGAGAGATCACCGTATGCGCGCGCG 18419
QY 1152 TACTCAGGATGATCGCGGGTGGCATCGTTCGAGCGCGTTCGCGCGAGCATGATCTCC 1211
Db 18420 AATCTCGCAGGATGTCTCCCTGCGGTGCGTATCCCTGTCGACGACGATCACTTCG 18479
QY 1212 ACCGGGAAGTCTGGTTG 1228
Db 18480 ACGGCTGATAGTCTG 18496

RESULT 11

US-10-858-730-133/c

; Sequence 133, Application US/10858730

; Publication No. US20050255568A1

; GENERAL INFORMATION:

; APPLICANT: Bailey, Richard B.

; APPLICANT: Blomquist, Paul

; APPLICANT: Doten, Reed

; APPLICANT: Driggers, Edward M.

; APPLICANT: Madden, Kevin T.

; APPLICANT: O'Leary, Jessica

; APPLICANT: O'Toole, George

; APPLICANT: Trueheart, Joshua

; APPLICANT: Walbridge, Michael J.

; APPLICANT: Yorgey, Peter S.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID

; FILE OF INVENTION: PRODUCTION

; FILE REFERENCE: 14184-030001

; CURRENT APPLICATION NUMBER: US/10/858,730

; CURRENT FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/475,000

; PRIOR FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: US 60/551,860

; PRIOR FILING DATE: 2004-03-10

; NUMBER OF SEQ ID NOS: 364

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 133

; LENGTH: 1386

; TYPE: DNA

; ORGANISM: Streptomyces coelicolor

US-10-858-730-133

Query Match 3.2%; Score 49.6; DB 8; Length 1386;

Best Local Similarity 44.0%; Pred. No. 0.0022;

Matches 263; Conservative 0; Mismatches 329; Indels 6; Gaps 1;

QY 682 CTTGGCGTGGCGGATACAGGCGCATGGTTCGGGCAACATGGCGATTCGCCATGCA 741
Db 916 CGTCAGCGCGCGCGCTCGACTCTTGATCTGTTGAGCAGTTCGAGTTCGATCCCT 857
QY 742 CCGCGTTCGCGAGTGCAGATACAGTCCAGGGGCATGACGTCCAGGAGTTCGCGAGAAATGTCGT 801
Db 856 TCTCGTCGACGACGTAGCCGAGGAGTCCGAGCGGTGACCGGCTTGGCGCGCGGCG 797
QY 802 ACGGCTTCGAGGCGCAGGTACAGCGCGAGTTGGTCTGGATGAAGTTTCATCAGATCAACG 861
Db 796 TCAGCTTCTCGATGTTGATAGTCGCCACGTTGCCGAGCCGAGAGCAGCCGCGTCTGGC 737
QY 862 CATTCAGGCTCAAGTTGCCCGCACCCGAAACCGGGGGAACTTCGAGTCTTTGGCATGGC 921
Db 736 CTTCCAGGTCTTCGCGCGCTCCGAGCATCGCGCGCGGAAACAGCAGTTCGCCGTAGC 677
QY 922 CFTCTCCCATATCACTCGGACGGGATGAAACACACCGTCTGTTGGGGTTCGGTTCGA 981
Db 676 CGGTGCGCTTCGGGGGATCAGCAGCGCCCGCCAGCCCTTGGCCCTTTCGCGGTTCAGGACGC 617

Qy	982	CGAATCGGACCTGTTTCTTAGCTTTCAGCGGATCGATCCAGTAGTGTGTCGCGCTCGCAC	1041
Db	616	CGGACTCCAGCGGTGTGTCATCGCGCGGTACTGCGCGAAGAGTAGCCGATCTTCGCGGC	557
Qy	1042	ACGCGAGTACTCGCCGCGAGCGCCGACAGGGCGCGGTACAGTTCCTCATTTAGAGCCGA	1101
Db	556	CCCCGA-----CGCCGATGTCCCCCGCGGAGCTCGTGTCTCGCGATGTGCCGCT	503
Qy	1102	GGTTTTCGGTCCTGAAGATCGGCGGGAACAGTGCGGGTACCGCTCGGCGTACTCACGGA	1161
Db	502	ACAGCTCCGTCACTAAGGACTGGCAGAACCGCATGACTCTCGCGTCGCTGCGCCGCTGCG	443
Qy	1162	TGATCGCGGGGTGGCATCGGTGCAGCGCTGTCGGCGAGCATGATCTTCACCGGGAAGT	1221
Db	442	GGTGGAAGTCGTGCGCCCTTGCGCGCGCGGATCCGAGCGCGGTACAGCGCTTTCTTGA	383
Qy	1222	CGGTTTCTGGTCGAGAAAGCTGTGCAAGGCGCTGACGGGCGTAGCCCCCTGGTTGTG	1279
Db	382	AGATCTCTCGAAGCCGAGGAACCTTGATGACGCCCAGGTTGACGGAACGGATGGAAGCG	325

RESULT 12

US-11-075-185-35/c
; Sequence 35, Application US/11075185
; Publication No. US20050266434A1

; GENERAL INFORMATION:
 ; APPLICANT: REEVES, CHRISTOPHER D
 ; APPLICANT: JULIEN, BRYAN
 ; APPLICANT: REID, RALPH

; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS

; FILE REFERENCE: 010099.03

; CURRENT APPLICATION NUMBER: US/11/075,185

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/551,103

; PRIOR FILING DATE: 2004-03-08

; PRIOR APPLICATION NUMBER: US 60/568,290

;
PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 35

; LENGTH: 10968

TYPE: DNA

ORGANISM: Sorangium cellulosum

US-11-075-185-35

Query Match	3.1%	Score 47.2	DB 12	Length 10968
Best Local Similarity	45.8%	Pred. No. 0.01		
Matches 163	Conservative	0	Mismatches 193	Indels 0
				Gaps 0

Qy	335	GAGCCGGAGGGCCACATCCACGAGCCGCCCTCGCGCTCGCGCTCGCGCGCGAGCTT	394
Db	9039	GCCTCTCGCGCCCGAGCGCGCACCCCGTCCGTGCTGTCGCCCGCGCTCGAA	8980
Qy	395	GCGGCATCGGTCATTGAGCCGCGCGGCGGTGTGCCCCGCGGTGCTGACAGCCACGAT	454
Db	8979	CGCCCCACGCGCGCGACCGCGCCCGCTCGCGCTCGCGAGGTGGATGACGCGCGTGAG	8920
Qy	455	GGCGATCCGGGGATGGCGCGGATGTTCTCTGACGCGCGCGCGCCCTCCGGGCGCTGG	514
Db	8919	CCCCCTCCCGTCTCTCGGCGCTGTTCTGAGCGGACGCGACCTCCCGTGCCTCCCGCG	8860
Qy	515	AACGTTGGCGATCTGGCGAAGGATCCAGTCGGCCATGACGCGCATGAGCTCTCGCGCGC	574
Db	8859	CGCTCGATCAGACGTCCTCGNGAACGGACGCCAGCAGCACCATTGCTGTCGCGACGC	8800
Qy	575	GGGGTCTCCCGGGAAACGAGTCGAGCATCGGCTCAAACGTCGCGGCATGCCCGGACCGCTG	634
Db	8799	CTCCTCTCGGCGACCGCGCCACGACGAGTGCAGCACCCGCTCGACGAGCGCCGATG	8740
Qy	635	CGTCAACCAAGATTTTGGGGGTCCACCACTGGTTGTGCCAATGCTTTGGGGGT	690
Db	8739	GATCCCGAAGCTCTGCGCCGTGTCCGCGACCGGCTCGGGACGCGGACCCGCGCGT	8684

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QY 301 CGGGGAGACGTCGATGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGAGACGTCGATGCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCGCATTTGACAA 420
Db 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCGCATTTGACAA 420
QY 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTTCGCGTTCCAAATCGACGCCG 480
Db 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTTCGCGTTCCAAATCGACGCCG 480
QY 481 GGGGTGCGGTGCTTCGAGTTTCGATCGGTAGTAAACGGGCCACGTTCAGCGAGCATGT 540
Db 481 GGGGTGCGGTGCTTCGAGTTTCGATCGGTAGTAAACGGGCCACGTTCAGCGAGCATGT 540
QY 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGTGGCTGG 600
Db 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGTGGCTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTGCATGCGAGGCTGGCGGGCAATGACCCAAAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTGCATGCGAGGCTGGCGGGCAATGACCCAAAA 660
QY 661 CCGCGCGGACGCTTCGCGGACGCAAGAGCGGTGGAGAGATAGATAATTTCACTGGCGA 720
Db 661 CCGCGCGGACGCTTCGCGGACGCAAGAGCGGTGGAGAGATAGATAATTTCACTGGCGA 720
QY 721 CAGTACTCAAAATAGTCCGGAGCCTCGGCTCGGACGTTAAAGAGCAGATCCAGAAATCCGAC 780
Db 721 CAGTACTCAAAATAGTCCGGAGCCTCGGCTCGGACGTTAAAGAGCAGATCCAGAAATCCGAC 780
QY 781 ACGGGGGCTCGAAACCTCCCACAATTCGTTATATATCGCGGTAGCCGTCATAATCGAAC 840
Db 781 ACGGGGGCTCGAAACCTCCCACAATTCGTTATATATCGCGGTAGCCGTCATAATCGAAC 840
QY 841 CAAGTTACCGGATGCTAAGTTGCTGCAACGCGCTCATCGACATACCAACGGGCTGAG 900
Db 841 CAAGTTACCGGATGCTAAGTTGCTGCAACGCGCTCATCGACATACCAACGGGCTGAG 900
QY 901 GGGCCAGAGACATATTCGGTCTGCGCGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 901 GGGCCAGAGACATATTCGGTCTGCGCGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
QY 961 TTGCGCTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCTGATACCGAGATAA 1020
Db 961 TTGCGCTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCTGATACCGAGATAA 1020
QY 1021 CTGCAAAATCGCATTCAATAGACGCTGTGAGTTAGGAAAGATTGCTGTGCTGTTCTCG 1080
Db 1021 CTGCAAAATCGCATTCAATAGACGCTGTGAGTTAGGAAAGATTGCTGTGCTGTTCTCG 1080
QY 1081 AGGTAATTCGGCGCAGGACAGTCAGCGATCTCCGCAAAATGAGCGGCCGCGCTGTAGTTG 1140
Db 1081 AGGTAATTCGGCGCAGGACAGTCAGCGATCTCCGCAAAATGAGCGGCCGCGCTGTAGTTG 1140
QY 1141 AATTCGTAGTCCCGCAGTGCGCTTTCGCCCAATTCGGTCCGTCGATCAGCGTCTCACGT 1200
Db 1141 AATTCGTAGTCCCGCAGTGCGCTTTCGCCCAATTCGGTCCGTCGATCAGCGTCTCACGT 1200
QY 1201 ATCTTTTGAATGAAAGCTCCCTTCACTCGGAGCGGAAAGATTATCCACTGTAAACCCCTGG 1260
Db 1201 ATCTTTTGAATGAAAGCTCCCTTCACTCGGAGCGGAAAGATTATCCACTGTAAACCCCTGG 1260
QY 1261 CTCTGTTTTCGATTCGATTTCTGTTCCCAATCACGCTTCGTTATTTGCAATGATCATAG 1320
Db 1261 CTCTGTTTTCGATTCGATTTCTGTTCCCAATCACGCTTCGTTATTTGCAATGATCATAG 1320
QY 1321 ATGATGAATTCATCGACGAATCGAATCAGGTCAAAATATCTCGCAAGGTATGTAATTT 1380
Db 1321 ATGATGAATTCATCGACGAATCGAATCAGGTCAAAATATCTCGCAAGGTATGTAATTT 1380
QY 1381 GATTGACAAATCGCGACTTCTTCAAC 1407
```

Db 1381 GATTGACAAATCGCGACTTCTTCAAC 1407

RESULT 2

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US-09-670-314-1
; Sequence 1, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-1
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Query Match 100.0%; Score 1407; DB 3; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACCTCGCTTCGAGAGATCAAAATAGGCGCATGGGTACGATAGTACAGGTGTCGTCGCA 60
Db 1 ACCTCGCTTCGAGAGATCAAAATAGGCGCATGGGTACGATAGTACAGGTGTCGTCGCA 60
QY 61 TCTTTGATGATCGGAATTAAGATGTCAAGCAATTAAGAGAGAGCCAGCGCATCGCG 120
Db 61 TCTTTGATGATCGGAATTAAGATGTCAAGCAATTAAGAGAGAGCCAGCGCATCGCG 120
QY 121 CATTGAGCATGTCGAGCGTCGCTTCGATGTAGCGCACCATTCGCTGTCACAGATTCA 180
Db 121 CATTGAGCATGTCGAGCGTCGCTTCGATGTAGCGCACCATTCGCTGTCACAGATTCA 180
QY 181 GACGAACATTGAATATTCACCTCGCGACGCTATAGTCCGCTCCGATCTATGCGCGCG 240
Db 181 GACGAACATTGAATATTCACCTCGCGACGCTATAGTCCGCTCCGATCTATGCGCGCG 240
QY 241 CGCAGATGAAGTCTCGGTCGCGCACCTTCGAAACGTAGTGGCGCGCGCGCACCATTT 300
Db 241 CGCAGATGAAGTCTCGGTCGCGCACCTTCGAAACGTAGTGGCGCGCGCGCACCATTT 300
QY 301 CGGGGAGACGTCGATGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGACGTCGATGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCGCATTTGACAA 420
Db 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCGCATTTGACAA 420
QY 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTTCGCGTTCCAAATCGACGCCG 480
Db 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTTCGCGTTCCAAATCGACGCCG 480
QY 481 GGGGTGCGGTGCTTCGAGTTTCGATCGGTAGTAAACGGGCCACGTTCAGCGAGCATGT 540
Db 481 GGGGTGCGGTGCTTCGAGTTTCGATCGGTAGTAAACGGGCCACGTTCAGCGAGCATGT 540
QY 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGTGGCTGG 600
Db 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGTGGCTGG 600
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Qy	601	GTCCGAGCTACTACCTTCAA	CAGTTGCATGCGGAGGCTGCGCGGGCAATGACCCAAAA	660		
Db	601	GTCCGAGCTACTACCTTCAA	CAGTTGCATGCGGAGGCTGCGCGGGCAATGACCCAAAA	660		
Qy	661	CCCCCGGCACGGTTCCGCGAGCAAGGCGTCGAGACGATAGATAATTTCACTGGCGA	720			
Db	661	CCCCCGGCACGGTTCCGCGAGCAAGGCGTCGAGACGATAGATAATTTCACTGGCGA	720			
Qy	721	CAGTACCTCAAAATAGTCGGAGCCCTCGGCTCCGAGCTTTAAAGAGCAGATCCAGAAATCGAC	780			
Db	721	CAGTACCTCAAAATAGTCGGAGCCCTCGGCTCCGAGCTTTAAAGAGCAGATCCAGAAATCGAC	780			
Qy	781	ACGCGGGCTCGAAACCTTCCCCACAAATTGCTTTATAATCGCGGTAGCGTCAATATCGAAC	840			
Db	781	ACGCGGGCTCGAAACCTTCCCCACAAATTGCTTTATAATCGCGGTAGCGTCAATATCGAAC	840			
Qy	841	CAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAACGGGCTGAG	900			
Db	841	CAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAACGGGCTGAG	900			
Qy	901	GGGCCAGAGACATATTCCGTGCTGCGGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC	960			
Db	901	GGGCCAGAGACATATTCCGTGCTGCGGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC	960			
Qy	961	TTGCGCTCGGCTAATTCGTAGTCCACGAAATTCGCCAGTCCGCTGATACCGAGATAA	1020			
Db	961	TTGCGCTCGGCTAATTCGTAGTCCACGAAATTCGCCAGTCCGCTGATACCGAGATAA	1020			
Qy	1021	CTGCAAAATCGCATTCAAATAGACGCTGTTCAGTAAAGGAAAGATTTCGTGCTGTTCTTCG	1080			
Db	1021	CTGCAAAATCGCATTCAAATAGACGCTGTTCAGTAAAGGAAAGATTTCGTGCTGTTCTTCG	1080			
Qy	1081	AGGTAATTCGGCGGAGCCAGTCAGCATCTCCGCAAAATGAGCGCGCGCTGTAGTTG	1140			
Db	1081	AGGTAATTCGGCGGAGCCAGTCAGCATCTCCGCAAAATGAGCGCGCGCTGTAGTTG	1140			
Qy	1141	AAATTCTAGTGC	CGCCAGTCGGCTTCGCCC	AAATCGGTCGATCAGCGTCTCACGT	1200	
Db	1141	AAATTCTAGTGC	CGCCAGTCGGCTTCGCCC	AAATCGGTCGATCAGCGTCTCACGT	1200	
Qy	1201	ATCTTTTGTATGGAAACGTCCTTCACCTGACGGGAA	CAGTTATCCA	CTGTAA	CCCCCTGG	1260
Db	1201	ATCTTTTGTATGGAAACGTCCTTCACCTGACGGGAA	CAGTTATCCA	CTGTAA	CCCCCTGG	1260
Qy	1261	CTCGTTTTGTATCCGATTTCTGTTTCGCGCAATCAGCTTGGTATATTCGATGTCATCATAG	1320			
Db	1261	CTCGTTTTGTATCCGATTTCTGTTTCGCGCAATCAGCTTGGTATATTCGATGTCATCATAG	1320			
Qy	1321	ATGATGAATTCATCGACGAATGCAATCAGGTCAAAATATCTCTGCCAAGGTATGTAATTT	1380			
Db	1321	ATGATGAATTCATCGACGAATGCAATCAGGTCAAAATATCTCTGCCAAGGTATGTAATTT	1380			
Qy	1381	GATTGAACAAATCGGACTTTCTTCAAC	1407			
Db	1381	GATTGAACAAATCGGACTTTCTTCAAC	1407			

RESULT 3

```

US-09-103-840A-2
; Patent 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

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QY 901 RGGCCAGAGACATATTCGGTCGTCGGCCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 1697049 GGGCCAGAGACATATTCGGTCGTCGGCCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 1697108
QY 961 TTGGCGTCGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
Db 1697109 TTGGCGTCGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1697168
QY 1021 CTGCAAAATCGCAATCAATAGACCCCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1080
Db 1697169 CTGCAAAATCGCAATCAATAGACCCCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1697228
QY 1081 AGGTAATCGGCGCGAGCCAGTCAGGATCTCCGCAAAATGAGCGCCCGCTGTAGTTG 1140
Db 1697229 AGGTAATCGGCGCGAGCCAGTCAGGATCTCCGCAAAATGAGCGCCCGCTGTAGTTG 1697288
QY 1141 AATCTAGTGC CGCGCAGTGGCTTTCCGCCCAATCGTCCGCTCGCATCAGCTCTCACGT 1200
Db 1697289 AATCTAGTGC CGCGCAGTGGCTTTCCGCCCAATCGTCCGCTCGCATCAGCTCTCACGT 1697348
QY 1201 ATCTTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1260
Db 1697349 ATCTTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1697408
QY 1261 CTCGTTTTGATCGGATTCCTGTTTGGCCAAATCAGCTTGGTATATGCAATGATCATATAG 1320
Db 1697409 CTCGTTTTGATCGGATTCCTGTTTGGCCAAATCAGCTTGGTATATGCAATGATCATATAG 1697468
QY 1321 ATGATGAATTCATCGACGAATCAATCAGTCAAAATATCCTCGCCAAAGTATGTAATTT 1380
Db 1697469 ATGATGAATTCATCGACGAATCAATCAGTCAAAATATCCTCGCCAAAGTATGTAATTT 1697528
QY 1381 GATTGAACAAATCGGCACTTTCTTCAAC 1407
Db 1697529 GATTGAACAAATCGGCACTTTCTTCAAC 1697555

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 1407; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGCTTGAGAGATCAATAGGCGCGCTGGTTCAGATAGTACAGGTCTGTCGCGCA 60
Db 1696015 ACCTGGCTTGAGAGATCAATAGGCGCGCTGGTTCAGATAGTACAGGTCTGTCGCGCA 1696074
QY 61 TCTTTGATCGATCGGAATAGATGTGAGGCAATTTAAAGAGAAGCCACCGCGACTCGCGG 120
Db 1696075 TCTTTGATCGATCGGAATAGATGTGAGGCAATTTAAAGAGAAGCCACCGCGACTCGCGG 1696134

QY 121 CATTGAGCATGTCGAGCGTCGCTTCGATGTCGAGCGACCAATTCGCTGTCCAAACGATTTC 180
Db 1696135 CATTGAGCATGTCGAGCGTCGCTTCGATGTCGAGCGACCAATTCGCTGTCCAAACGATTTC 1696194
QY 181 GACGAAACATTTGAATATTTCCACTCGCGAGAGCTATAGTCCGCTCCCGATCTATGCGCGCG 240
Db 1696195 GACGAAACATTTGAATATTTCCACTCGCGAGAGCTATAGTCCGCTCCCGATCTATGCGCGCG 1696254
QY 241 CGCAGATGAAGTCTCGGTTTCGCCCGACCTTCCAAAGAGTGTAGTGGCGCGCGGACCAATTT 300
Db 1696255 CGCAGATGAAGTCTCGGTTTCGCCCGACCTTCCAAAGAGTGTAGTGGCGCGCGGACCAATTT 1696314
QY 301 CGGGGAGAGCTCGATCGCGGTGTAATCAGTTTTGAAAGCCACGCGCATCTAGTAGTCCA 360
Db 1696315 CGGGGAGAGCTCGATCGCGGTGTAATCAGTTTTGAAAGCCACGCGCATCTAGTAGTCCA 1696374
QY 361 GTAGAGCCCATAGCAGCCTAGATCGTTGATCGAAATGGGTCCGCGCATTTGACAAA 420
Db 1696375 GTAGAGCCCATAGCAGCCTAGATCGTTGATCGAAATGGGTCCGCGCATTTGACAAA 1696434
QY 421 TCGGCAACAGCTGTGTCAAAGCGCAACGCTGCCCGCTTCGCGCTTCCAAATCGACCGCG 480
Db 1696435 TCGGCAACAGCTGTGTCAAAGCGCAACGCTGCCCGCTTCGCGCTTCCAAATCGACCGCG 1696494
QY 481 GCGGGTGCCTGCTCGAGTTTCGATGCGTAGTAAACGGGCCACGTCAGCGAGCATGTT 540
Db 1696495 GCGGGTGCCTGCTCGAGTTTCGATGCGTAGTAAACGGGCCACGTCAGCGAGCATGTT 1696554
QY 541 CTTTCGCTCTTCCGCATGAAGCTGCTCACGATTTGTGTGTGGGCTCGGTCGCTGG 600
Db 1696555 CTTTCGCTCTTCCGCATGAAGCTGCTCACGATTTGTGTGTGGGCTCGGTCGCTGG 1696614
QY 601 GTCCGAGACTATACCTTCAACAGTTGCAATGTCGAGGCTCGCGGGGCAATGACCCAAAA 660
Db 1696615 GTCCGAGACTATACCTTCAACAGTTGCAATGTCGAGGCTCGCGGGGCAATGACCCAAAA 1696674
QY 661 CCGCGCGGACAGTTTCGCGGAGCAAGGAGCGTGGAGACATAGATAATTTTCACTGCGCA 720
Db 1696675 CCGCGCGGACAGTTTCGCGGAGCAAGGAGCGTGGAGACATAGATAATTTTCACTGCGCA 1696734
QY 721 CAGTACCTCAAAATAGTTCGCGAGCTCGGCTCCGAGCTTAAAGAGCAGATCCAGAAATCGAC 780
Db 1696735 CAGTACCTCAAAATAGTTCGCGAGCTCGGCTCCGAGCTTAAAGAGCAGATCCAGAAATCGAC 1696794
QY 781 ACGCGGGCTCGAAACCTCCCAATTTGCTTATTAATTCGCGGTAGCGCTCATATCGAAC 840
Db 1696795 ACGCGGGCTCGAAACCTCCCAATTTGCTTATTAATTCGCGGTAGCGCTCATATCGAAC 1696854
QY 841 CAAAGTTACCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 900
Db 1696855 CAAAGTTACCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 1696914
QY 901 GGGCCAGAGACATATTCGGTCGCTCGCGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 1696915 GGGCCAGAGACATATTCGGTCGCTCGCGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 1696974
QY 961 TTGCGCTCGGCTAAATTCGTAGTCCCAACGAAATTTGCGAGTGTGCTGATACCGAGATAA 1020
Db 1696975 TTGCGCTCGGCTAAATTCGTAGTCCCAACGAAATTTGCGAGTGTGCTGATACCGAGATAA 1697034
QY 1021 CTGCAAAATCGCAATCAATAGACCGCTTGTAGTAAAGAAAGATTCGTGTGCTTCTTCG 1080
Db 1697035 CTGCAAAATCGCAATCAATAGACCGCTTGTAGTAAAGAAAGATTCGTGTGCTTCTTCG 1697094
QY 1081 AGGTAATCGGCGCGAGCCAGTCAGGATCTCCGCAAAATGAGCGCCCGCTGTAGTTG 1140
Db 1697095 AGGTAATCGGCGCGAGCCAGTCAGGATCTCCGCAAAATGAGCGCCCGCTGTAGTTG 1697154
QY 1141 AATCTAGTGC CGCGCAGTGGCTTTCCGCCAAATCGTCCGCTCGCATACGCTCTCACGT 1200
Db 1697155 AATCTAGTGC CGCGCAGTGGCTTTCCGCCAAATCGTCCGCTCGCATACGCTCTCACGT 1697214
QY 1201 ATCTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1260

Db 1697215 ATCTTTTGTGAAACGTCCTTCCCTGACGCGAAGAGTTATCCATGTAACCCCTGG 1697274
QY 1261 CTCGTTTTCATCCGATTTCTGTTTCCCAATCACGCTTCGTATATTGCGATGTCATCATAG 1320
Db 1697275 CTCGTTTTCATCCGATTTCTGTTTCCCAATCACGCTTCGTATATTGCGATGTCATCATAG 1697334
QY 1321 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1380
Db 1697335 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1697394
QY 1381 GATTGAACCAATCCGACATTTCTTCAAC 1407
Db 1697395 GATTGAACCAATCCGACATTTCTTCAAC 1697421

RESULT 5

US-09-894-844-44/c
; Sequence 44, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-44

Query Match 49.3%; Score 693; DB 3; Length 693;
Best Local Similarity 100.0%; Pred. No. 4.9e-216;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 714 CTGGGACAGTACCTCAATAGTCCGAGCCTCGGCTCCGAGCTTAAAGACAGATCCAG 773
Db 693 CTGGGACAGTACCTCAATAGTCCGAGCCTCGGCTCCGAGCTTAAAGACAGATCCAG 634
QY 774 AATCGACAGCGGGCTCGAACCCTCCCAATTCCTTATATCGGGTAGCGGTGCTATA 833
Db 633 AATCGACAGCGGGCTCGAACCCTCCCAATTCCTTATATCGGGTAGCGGTGCTATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTCTGTCGAACAGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTACCCGGATGTAAGTTCTGTCGAACAGCGCTCATCGACATACGAACG 514
QY 894 GCGTAGGGGCGCAGACATATTCGTCGCTCGCGCTGTGGCAGAGTTGGCCAGTCT 953
Db 513 GCGTAGGGGCGCAGACATATTCGTCGCTCGCGCTGTGGCAGAGTTGGCCAGTCT 454
QY 954 CTCGGTCTTCGGCTCGGCTAATTCGTAGTCCCAAGATTTGCCAGTCGGTGTGATACC 1013
Db 453 CTCGGTCTTCGGCTCGGCTAATTCGTAGTCCCAAGATTTGCCAGTCGGTGTGATACC 394
QY 1014 GAGATAACTGCAATCGCAATCAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 1073
Db 393 GAGATAACTGCAATCGCAATCAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 334
QY 1074 TTCTTCGAGTAAATCGGCGCGAGCGAGTCAGCATCTCCGCAAAATGAGCGCGCGCGCT 1133
Db 333 TTCTTCGAGTAAATCGGCGCGAGCGAGTCAGCATCTCCGCAAAATGAGCGCGCGCGCT 274

QY 1134 GTAGTTGAATTTCTAGTCCCGCAGTGCCTTTTCCGCAATCGGTCCCGTCCGATCAGCGT 1193
Db 273 GTAGTTGAATTTCTAGTCCCGCAGTGCCTTTTCCGCAATCGGTCCCGTCCGATCAGCGT 214
QY 1194 CTCAGGTATCTTTTGTATGAAACGTCCTTCCACCTGAGACGGGAAACAGTTATCCACTGTAA 1253
Db 213 CTCAGGTATCTTTTGTATGAAACGTCCTTCCACCTGAGACGGGAAACAGTTATCCACTGTAA 154
QY 1254 CCCCTGGCTCGTTTGTATCCGATTTCTGTTTCCGCAATCACGCTTGGTATATTGCAATGC 1313
Db 153 CCCCTGGCTCGTTTGTATCCGATTTCTGTTTCCGCAATCACGCTTGGTATATTGCAATGC 94
QY 1314 ATCATAGATGATGAATTTCAATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTAT 1373
Db 93 ATCATAGATGATGAATTTCAATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTAT 34
QY 1374 GTAAATTTGATGAACAAATCGGACTTTCTTCAA 1406
Db 33 GTAAATTTGATGAACAAATCGGACTTTCTTCAA 1

RESULT 6

US-09-894-844-43/c
; Sequence 43, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-43

Query Match 30.3%; Score 427; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.5e-129;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTCGGCTTGACAGATCAAAATAGGCGCATGGGTGACATAGTACAGGTCTCGCGCA 60
Db 427 ACTCGGCTTGACAGATCAAAATAGGCGCATGGGTGACATAGTACAGGTCTCGCGCA 368
QY 61 TCTTTGATCATCGGAATTAAGATGTCAGGCAATTAAGAGAGCCACCGCGACTCGCG 120
Db 367 TCTTTGATCATCGGAATTAAGATGTCAGGCAATTAAGAGAGCCACCGCGACTCGCG 308
QY 121 CATTCAGCATGTCGAGCGCTCGCTTCGATGTAGCGCACCATTTCCGTTGTCACAGATTCA 180
Db 307 CATTCAGCATGTCGAGCGCTCGCTTCGATGTAGCGCACCATTTCCGTTGTCACAGATTCA 248
QY 181 GACGAACATGTAATTTCCATCTCGGACGCTATAGTCGCGCTCCCGATCTATGCGGCGCG 240
Db 247 GACGAACATGTAATTTCCATCTCGGACGCTATAGTCGCGCTCCCGATCTATGCGGCGCG 188
QY 241 CGCAGATGAGTCTGGTTCCGCCGACCTTCGAAAGCTAGTCGGCGCGCGCGCACCATTT 300
Db 187 CGCAGATGAGTCTGGTTCCGCCGACCTTCGAAAGCTAGTCGGCGCGCGCGCACCATTT 128
QY 301 CGGGGAGACGTCGATGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360

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Db 127 CCGGGGAGACGTCGATCCGGTGATCATAGTTTGAAGCCACGCGCATCTAGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCCGATTGACAA 420
Db 67 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCCGATTGACAA 8
QY 421 TCGGCAC 427
Db 7 TCGGCAC 1

RESULT 7
US-09-543-681A-4167/c
; Sequence 4167, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4167
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4167

Query Match 3.6%; Score 50.4; DB 3; Length 702;
Best Local Similarity 55.8%; Pred. No. 9.2e-06;
Matches 96; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1234 GGAACAGTTATCCACTGTAAACCCTGGCTGTTTGTGATCGGATTTCTGTTTGCACATCA 1293
Db 173 GGAATAGTAAATAATTGTGGACCAATTTCTAGTTTGAATTCGATTTCTATTATATATCA 114
QY 1294 CGCTTGGTATATGCAATGTCATCATAGATGATGAATTCATCGACGAATGCAATCAGGTCA 1353
Db 113 CTTTAAATATAATTACATCATCAATAAATAATAATATATCGTATGATAAGCTAATTCGA 54
QY 1354 AAATATCTCGCCAGGTATGTAATTGATGAACAAATCGGACTTTCTTCA 1405
Db 53 TAATATCCTATATATGGAATAAGTAAGTTGCAATACAGCTAATATATCA 2

RESULT 8
US-09-949-016-13678
; Sequence 13678, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13678
; LENGTH: 18037
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13678
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Query Match 2.8%; Score 39.8; DB 3; Length 18037;
Best Local Similarity 48.1%; Pred. No. 0.17;
Matches 113; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 411 GCATTGACAATCGGCACACAGCTGGTCAAGCGCAACGCTGCGCGGCTTCGGCGTTCCAA 470
Db 3848 GCCTAGGGCTCGGCAGCTGTGACCAAGCGGGGCCACCTGCGCTCTGAGCCCTGCCAG 3907
QY 471 TCACGCCGCGCGGGTGGCTGTGCTTCCGATCGTAGTAACTGATCGTAGTAACTGATCGTAG 530
Db 3908 GTGACGCCGAGCCAGAGCCCTGGCGTGGAGGGTGAAGTGGCAGCCAGAGGGCTGGTGAG 3967
QY 531 CGAGCATGTCGTTGGCTTTCGGCCATGAAGTGCCTCAGATTTGTGTGTGTGTGGCGGT 590
Db 3968 AGTGGCTGTTTCTCCCAACAGCTGACTTTTGGGGTGTCAAGCGAGCTGACAGCGTCTGTGG 4027
QY 591 CGGTGCGTGGTCCGAGACTATACCTTCAACAGTTTGTCATGCCGAGGCTCGGCGG 645
Db 4028 CCAAGAGGAGGTCTTTCATTGGGACTCCCTACTGGTGAGGCTGGCCTGGGCGG 4082

RESULT 9
US-09-902-540-6354/c
; Sequence 6354, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6354
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6354

Query Match 2.5%; Score 35.8; DB 3; Length 702;
Best Local Similarity 56.3%; Pred. No. 0.55;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 203 CCGGAGGCTATAGTCGGCTCCGATCTATCGCGCGCGCAGATGAAGTCTCGGTTCCG 262
Db 225 CCGGTGGAACGACTCCGGCTCCGGAAGGATGCGCGGCTCGCACGAAGACGGGTCTC 166
QY 263 CCGACCTTCGAAACGTAGTGGCGCGCGCCACCAATTTCCGGGGAGACCTTCGATGCGG 321
Db 165 CAGCGCTCTCTCAGACACACCGCGCGCGGCTCTCTCTTTGGAGAAGCGGATGG 107

RESULT 10
US-09-902-540-408/c
; Sequence 408, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
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/ SEQ ID NO 408
/ LENGTH: 1583
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-408

Query Match          2.5%; Score 35.8; DB 3; Length 1583;
Best Local Similarity 56.3%; Pred. No. 0.87;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 203 CCGGACGCTATAGTCGCGCTCCCGATCTATGCGCGCGCGCAGATGAAGTCTCGGTTCCG 262
Db 1106 CCGGTGAAACGACTCGGCTCCGGAAGATGCGCGCGCTCGCACGAAGACGGGTCCTC 1047

QY 263 CCGACCTTCGAAACGTAAGTCGCGCGCGCGCACCATTTTCGGGGGAGACGTCGATGCCGG 321
Db 1046 CAGCCGCTCTCAGACACACCGCGCGCGGGGCTCTCTTGGAGAGAGCGGATGG 988

RESULT 11
US-09-949-016-16832/c
/ Sequence 16832, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16832
/ LENGTH: 5992
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16832

Query Match          2.5%; Score 35.8; DB 3; Length 5992;
Best Local Similarity 51.1%; Pred. No. 1.8; Indels 6; Gaps 1;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTTCAGGCAATTAAAGAGAGAGCCAGCGGACTCGCGGCATTCAGCATGTGCG 134
Db 3344 GAGGAAGCTGGGTACACACAGCCAGAGAGCGGGGAAACGGGGCATCTAACTAGGAC 3285.

QY 135 AGCGTCGCTTCCA-----TGTGAGCGCACCAATTCGTCGTCACGATTTTCAGACGAACA 188
Db 3284 ACAGTCGCATCCAGGGGTGAGTACCTGACCTTACAGGCGCCACCACTTCAGACTGAGA 3225

QY 189 TTGAATATTCCACTCGCGAGCTATAGTCGCGCTCCCGATCTATGCGCGCGCGCAGATG 248
Db 3224 TGGAAACGCCCTCTGGAGAACCTGATCGCGCCACCTTACAGAGCCCGGAGGTACT 3165

QY 249 AAGTCTGCGCTTCGCGGACCTTCGAAACGTAAGTCGCGCGCGC 289
Db 3164 GGGCCTGCGCGCCACACCTTGGCCGCGAGTGGCCTCTGCG 3124

RESULT 12
US-09-949-016-16833
/ Sequence 16833, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16833
/ LENGTH: 8345
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16833

Query Match          2.5%; Score 35.8; DB 3; Length 8345;
Best Local Similarity 51.1%; Pred. No. 2.2;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTTCAGGCAATTAAAGAGAGAGCCAGCGGACTCGCGGCATTCAGCATGTGCG 134
Db 6980 GAGGAAGCTGGGTACACACAGCCAGAGAGCGGGGAAACGGGGCATCTAACTAGGAC 7039

QY 135 AGCGTCGCTTCCA-----TGTGAGCGCACCAATTCGTCGTCACGATTTTCAGACGAACA 188
Db 7040 ACAGTCGCATCCAGGGGTGAGTACCTGACCTTACAGGCGCCACCACTTCAGACTGAGA 7099

QY 189 TTGAATATTCCACTCGCGAGCTATAGTCGCGCTCCCGATCTATGCGCGCGCGCAGATG 248
Db 7100 TGGAAACGCCCTCTGGAGAACCTGATCGCGCCACCTTACAGAGCCCGGAGGTACT 7159

QY 249 AAGTCTGCGCTTCGCGGACCTTCGAAACGTAAGTCGCGCGCGC 289
Db 7160 GGGCCTGCGCGCCACACCTTGGCCGCGAGTGGCCTCTGCG 7200

RESULT 13
US-09-902-540-3161/c
/ Sequence 3161, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 3161
/ LENGTH: 978
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-3161

Query Match          2.5%; Score 35.6; DB 3; Length 978;
Best Local Similarity 57.0%; Pred. No. 0.77;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 215 GTCCGCTCCCGATCTATGCGCGCGCGCAGATGAAGTCTGCGTTCGCGCGCACCTTCGAA 274
Db 531 GTCCGCTTCGCTCGCTCAGCTCACCAGCGCATGACGCGTTCGCGCGCGCGCCAC 472

QY 275 ACGTAGTGGCGCGCGCGCACCACTTCGGGGGAGAGCTCGATGCCGCTGTAATC 328
Db 471 CTGCACCGCGCGCGTGGCCACGCTCCCGCGCGCATGACACGACGCTCTC 418
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RESULT 14
US-09-902-540-1144
; Sequence 1144, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1144
; LENGTH: 16350
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
;
US-09-902-540-1144

Query Match          2.5%; Score 35.6; DB 3; Length 16350;
Best Local Similarity 57.0%; Pred. No. 3.8;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 215 GTCGCGCTCCGATCTATGCGCGCGCGAGATGAAGTCTGCGTTGCGCCGACCTTCGAA 274
      |||||
Db 3602 GTCGCGCTTGGCTGCTGCTCACCACGCGGATGACGCGTGTGCGCGCGCGGCCAC 3661

QY 275 ACGTAGTGGCGCGCGCGACCATTTTCGGGGGAGAGCTGATGCGCGTGTATC 328
      |||||
Db 3662 CTGCACCGCGCGCGTGTGCCACGCTCTCCGCGGCGCATGGACACGACGCTCTC 3715

RESULT 15
US-09-949-016-177875
; Sequence 177875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177875
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-177875

Query Match          2.5%; Score 35.4; DB 3; Length 601;
Best Local Similarity 50.7%; Pred. No. 0.68;
Matches 112; Conservative 1; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTACGGCAATTAAGAGAGAGCCACGCGGACTCGCGCATTCAGCATGTCG 134
      |||||
Db 218 GAGGAGCTGGGTCTACACAGCCAGAGAGGGGGAAACGGGCACTCTAAGTAGGAC 277

QY 135 AGCGTCGCTTCGA-----TGTGAGCGCACCAATTCGTTCCAAACGATTTACAGACGAACA 188
      |||||
Db 278 ACAGTCGCATCCAGGGGTGAGTCRCCTGACCTACAGGGGCCACCACTTCAGACTGAGA 337

QY 189 TTGAATATTCACCTCGCAGGCTATAGTCGGCTCCCGATCTATGCGCGCGCGCAGATG 248
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Db 338 TGGAAACGCCCTCTTGGGAGAACCTGTATCCGCCCCACCCCTACACAGGCCCGGAGGTACT 397
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QY 249 AAGTCTGCGTTGCGCCCGACCTTCGAAACGTAGTGGGGCGC 289
      |||||
Db 398 GGGCTTGGCGCGCCACACCTTGGCGCGGAGTGGGCTCTGC 438
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Searched: 9793542 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

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10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1407	100.0	12732	6	US-10-259-678-1
2	693	49.3	693	3	US-09-894-844-44
3	693	49.3	693	7	US-10-388-902-44
4	693	49.3	693	7	US-10-647-089-44
5	427	30.3	498	3	US-09-894-844-43
6	427	30.3	498	7	US-10-388-902-43
7	427	30.3	498	7	US-10-647-089-43
8	39.8	2.8	27204	5	US-10-087-192-1528
9	38.4	2.7	2464	9	US-10-521-103-1
10	37.8	2.7	536	7	US-10-338-110-119
11	37.8	2.7	894	6	US-10-156-761-1933
12	37.8	2.7	9025608	6	US-10-156-761-1
13	36.6	2.6	485	7	US-10-437-963-48583
14	36.2	2.6	783	6	US-10-156-761-2972
15	36	2.6	1126	7	US-10-425-114-34546
16	36	2.6	1188	8	US-10-425-115-62490
17	35.8	2.5	17138	8	US-10-741-600-18009
18	35.6	2.5	1662	7	US-10-437-963-12650
19	35.4	2.5	622	4	US-09-925-065A-597843
20	35.4	2.5	727	9	US-10-956-157-3059
21	35.4	2.5	727	9	US-10-956-157-8294
22	35.4	2.5	1632	6	US-10-369-493-38385
23	35.4	2.5	4698	6	US-10-156-761-6923

C	24	35.4	2.5	9025608	6	US-10-156-761-1	Sequence 1, Appli
C	25	35.2	2.5	3683	6	US-10-369-493-35076	Sequence 35076, A
C	26	35	2.5	459	8	US-10-627-592-16	Sequence 16, Appl
C	27	35	2.5	1215	6	US-10-321-188-72	Sequence 72, Appl
C	28	35	2.5	1215	6	US-10-321-188-74	Sequence 74, Appl
C	29	35	2.5	1215	9	US-10-915-172-72	Sequence 72, Appl
C	30	35	2.5	1215	9	US-10-915-172-74	Sequence 74, Appl
C	31	35	2.5	1266	6	US-10-369-493-39313	Sequence 39313, A
C	32	35	2.5	1269	6	US-10-369-493-39688	Sequence 39688, A
C	33	35	2.5	1269	6	US-10-369-493-40041	Sequence 40041, A
C	34	35	2.5	1545	9	US-10-200-545-48	Sequence 48, Appl
C	35	34.8	2.5	1540	8	US-10-425-115-167794	Sequence 167794, A
C	36	34.8	2.5	1554	7	US-10-282-122A-14480	Sequence 14480, A
C	37	34.6	2.5	388	4	US-09-925-065A-585977	Sequence 585977, A
C	38	34.6	2.5	496	4	US-09-925-065A-827710	Sequence 827710, A
C	39	34.6	2.5	671	5	US-10-184-644-346	Sequence 346, App
C	40	34.6	2.5	671	5	US-10-184-634-346	Sequence 346, App
C	41	34.6	2.5	810	7	US-10-767-701-9705	Sequence 9705, Ap
C	42	34.6	2.5	939	7	US-10-282-122A-13932	Sequence 13932, A
C	43	34.4	2.4	328	8	US-10-674-124A-5740	Sequence 5740, Ap
C	44	34.4	2.4	963	6	US-10-369-493-38385	Sequence 38385, A
C	45	34.4	2.4	963	6	US-10-369-493-38868	Sequence 38868, A

ALIGNMENTS

RESULT 1

US-10-259-678-1
; Sequence 1, Application US/10259678
; Publication No. US20030198974A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/10/259,678
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-259-678-1

Query Match	100.0%	Score 1407;	DB 6;	Length 12732;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1407;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACCTCGCTTCGAGAGATCAAAATAGCGGCATCGGTGATAGTACAGGTGTCGCGCA	60	
Db	1	ACCTCGCTTCGAGAGATCAAAATAGCGGCATCGGTGATAGTACAGGTGTCGCGCA	60	
Qy	61	TCCTTTGATGATCGCAATAAGATGTCAGCAATTAAGAGAGAACGACGCGGCTCGCGG	120	
Db	61	TCCTTTGATGATCGCAATAAGATGTCAGCAATTAAGAGAGAACGACGCGGCTCGCGG	120	
Qy	121	CATTGAGATGTCGAGCGTGGCTTCGATGTGAGCGCACCATTCGCTGTCACAGATTTC	180	
Db	121	CATTGAGATGTCGAGCGTGGCTTCGATGTGAGCGCACCATTCGCTGTCACAGATTTC	180	
Qy	181	GACGAACTTGAATTCATCTCGGAGAGCTATAGTCCGCTCCGATCTATGTCGCGCGG	240	
Db	181	GACGAACTTGAATTCATCTCGGAGAGCTATAGTCCGCTCCGATCTATGTCGCGCGG	240	
Qy	241	CGCAGATGATGCTCGGTTCGCCCGACCTTCGAAACGATAGTGGCGCGCGCACCATTT	300	

Db 241 |||||CGCAGATGAAGTCTGGGTTGCGCCGACCTTCGAAAGCTAGTGGGCGCGCCGACCATTT 300
QY 301 CGGGGAGACGTCGATGCGCGGTGAATAGTTTTGAAGCCACGCGCATCTAGGTAGTCCA 360
Db 301 CGGGGAGACGTCGATGCGCGGTGAATAGTTTTGAAGCCACGCGCATCTAGGTAGTCCA 360
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTTGNATCGAAAATGGTCCGCGCATTTGACAA 420
Db 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTTGNATCGAAAATGGTCCGCGCATTTGACAA 420
QY 421 TCGCACACAGCTGGTCAAAAGCGCAACGCGCTGCCGCTTTCGCGTTTCCCAATCGAGCGCG 480
Db 421 TCGCACACAGCTGGTCAAAAGCGCAACGCGCTGCCGCTTTCGCGTTTCCCAATCGAGCGCG 480
QY 481 CGGGGTGCGGTGCTGCTTCGAGTTTTGATGCTGAGTAAACGCGGCCACGTCAGCGAGCATGGT 540
Db 481 CGGGGTGCGGTGCTGCTTCGAGTTTTGATGCTGAGTAAACGCGGCCACGTCAGCGAGCATGGT 540
QY 541 CGTTGGTCTTCCGCCATGAAGTGGCTCAGATTTGTGTGTGGGCGTCCGGTGGTGG 600
Db 541 CGTTGGTCTTCCGCCATGAAGTGGCTCAGATTTGTGTGTGGGCGTCCGGTGGTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGCTGCGGCGGCAATGACCCAAAAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGCTGCGGCGGCAATGACCCAAAAA 660
QY 661 CCGCGCGGCA CGGTTGCGCGAGCAAGAACGCTGGAGACGATAGATAATTTCACTGGCGA 720
Db 661 CCGCGCGGCA CGGTTGCGCGAGCAAGAACGCTGGAGACGATAGATAATTTCACTGGCGA 720
QY 721 CAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAGAAATCGAC 780
Db 721 CAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAGAAATCGAC 780
QY 781 ACGGGGGCTCGAACCTCCGCCACAAATTCCTTATATATCGCGGTAGCCGTCATAATCGCAC 840
Db 781 ACGGGGGCTCGAACCTCCGCCACAAATTCCTTATATATCGCGGTAGCCGTCATAATCGCAC 840
QY 841 CAAAGTTACCGGATGCTAAGTTCTGTCGAAACAGCGCTCATCGACATACGAAACGGGCTGAG 900
Db 841 CAAAGTTACCGGATGCTAAGTTCTGTCGAAACAGCGCTCATCGACATACGAAACGGGCTGAG 900
QY 901 GGGCCAGACACATATTCGTCGTCGCGGCTGTTGGCAGAGGTTGGCAGTCTCTCGGTC 960
Db 901 GGGCCAGACACATATTCGTCGTCGCGGCTGTTGGCAGAGGTTGGCAGTCTCTCGGTC 960
QY 961 TTGCGCGTGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
Db 961 TTGCGCGTGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
QY 1021 CTGCAAAATCGCATTCAAATAGAGCGCTGTTGAGTAAAGAAAGATTCGTGTGCTGTTCTCG 1080
Db 1021 CTGCAAAATCGCATTCAAATAGAGCGCTGTTGAGTAAAGAAAGATTCGTGTGCTGTTCTCG 1080
QY 1081 AGGTAATTCGGCGGAGCGAGTCAGCATCTCCGAAAAATGAGCGCGCTGCTAGTTTG 1140
Db 1081 AGGTAATTCGGCGGAGCGAGTCAGCATCTCCGAAAAATGAGCGCGCTGCTAGTTTG 1140
QY 1141 AATTCGTAGTGGCGGAGTGGCTTTCGCCCAATCGGTGCGTCCGATCAGCGTCTCAAGT 1200
Db 1141 AATTCGTAGTGGCGGAGTGGCTTTCGCCCAATCGGTGCGTCCGATCAGCGTCTCAAGT 1200
QY 1201 ATCTTTTGATGAAACGTCCTTTCACTTGGACGGGAAACAGTTTATCCACTGTAAACCCCTGG 1260
Db 1201 ATCTTTTGATGAAACGTCCTTTCACTTGGACGGGAAACAGTTTATCCACTGTAAACCCCTGG 1260
QY 1261 CTCGTTTGATCCGATTTCTGTTTTCGCCCAATCAOGCTTGGTATATTCGATGTCATCATAG 1320
Db 1261 CTCGTTTGATCCGATTTCTGTTTTCGCCCAATCAOGCTTGGTATATTCGATGTCATCATAG 1320
QY 1321 ATGATCAATTCATCGACGAATGCAATCAGGTCAAAATATCCTTCGCCCAAGGTATGTAATTT 1380

Db 1321 ATGATCAATTCATCGACGAATCAATCAGGTCAAAATATCCTTCGCCCAAGGTATGTAATTT 1380
QY 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407
Db 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407
RESULT 2
US-09-894-844-44/c
; Sequence 44, Application US/098994844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-44
Query Match 49.3%; Score 693; DB 3; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 714 CTGGGCGACGATGACCTCAAAATAGTCCGGAGCCTCGGCTCCGAGCGTTAAAGAGCAGATCCAG 773
Db 693 CTGGGCGACGATGACCTCAAAATAGTCCGGAGCCTCGGCTCCGAGCGTTAAAGAGCAGATCCAG 694
QY 774 AATCGACACGCGGGCTCGAACCCCTCCACAAATTCCTTATATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGCGGGCTCGAACCCCTCCACAAATTCCTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAAACCAAGTTACCCGGATGCTAAGTTGTCGAAACACGCGCTCATCGACATACGAAACG 893
Db 573 ATCGAAACCAAGTTACCCGGATGCTAAGTTGTCGAAACACGCGCTCATCGACATACGAAACG 514
QY 894 GGCTGAGGGGCGAGAGACATATTCGGTCTCGCGGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGCTGAGGGGCGAGAGACATATTCGGTCTCGCGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTGGCGTGGCTAAATTCGTCAGTCCACAGAAATTCGCGTCCGCTGATACC 1013
Db 453 CTCGGTCTTGGCGTGGCTAAATTCGTCAGTCCACAGAAATTCGCGTCCGCTGATACC 394
QY 1014 GAGATAAATCGCAATTCGAATTCGAATAGACGCTGTTGAGTAAAGAAAGATTCGTGTGCTG 1073
Db 393 GAGATAAATCGCAATTCGAATTCGAATAGACGCTGTTGAGTAAAGAAAGATTCGTGTGCTG 334
QY 1074 TTCTTCGAGGTTAAATTCGGCGGAGCGAGTCAGCATCTCCGAAAAATGAGCGGCGCGCT 1133
Db 333 TTCTTCGAGGTTAAATTCGGCGGAGCGAGTCAGCATCTCCGAAAAATGAGCGGCGCGCT 274
QY 1134 GTAGTTGAATTCAGTGGCGGCGAGTGGCTTTCCGCCAATCGGTCCGCTCGATCAGCGT 1193
Db 273 GTAGTTGAATTCAGTGGCGGCGAGTGGCTTTCCGCCAATCGGTCCGCTCGATCAGCGT 214
QY 1194 CTCAGGTATCTTTTGNATGGAACAGTCCCTTTCACCTGGAGCGGAAACAGTTTATCCACTGTAA 1253
Db 213 CTCAGGTATCTTTTGNATGGAACAGTCCCTTTCACCTGGAGCGGAAACAGTTTATCCACTGTAA 154

QY 1254 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACAGCTTGATATATTCGATGTC 1313
Db 153 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACAGCTTGATATATTCGATGTC 94
QY 1314 ATCATAGATGATCAATTCATCGAGCAATCAATCAGTCAAAATATCTCGCCAAAGTAT 1373
Db 93 ATCATAGATGATCAATTCATCGAGCAATCAATCAGTCAAAATATCTCGCCAAAGTAT 34
QY 1374 GTAAATTTGATTGAACAATCCGACTTCTTCAA 1406
Db 33 GTAAATTTGATTGAACAATCCGACTTCTTCAA 1

RESULT 3
US-10-388-902-44/c
; Sequence 44, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE OF INVENTION: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-44

Query Match 49.3%; Score 693; DB 7; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAG 773
Db 693 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAG 634
QY 774 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTCGTCGAACAGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTACCCGGATGTAAGTTCGTCGAACAGCGCTCATCGACATACGAACG 514
QY 894 GGTGAGGGGCGCAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGTGAGGGGCGCAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGATTTGCCAGTCTGATATACC 1013
Db 453 CTGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGATTTGCCAGTCTGATATACC 394
QY 1014 GAGATAACTGCAATCGCAATTCATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 1073
Db 393 GAGATAACTGCAATCGCAATTCATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 334
QY 1074 TTCCTCGAGTTAATCGGCGCAGCAGTCCAGGATTCCTCGCAAAATAGCGCGCGCT 1133
Db 333 TTCCTCGAGTTAATCGGCGCAGCAGTCCAGGATTCCTCGCAAAATAGCGCGCGCT 274

QY 1134 GTAGTTGAATTCATAGTCCCGCAGTGCCTTTTCGCCAATACGCTCGCTCGATCAGCGT 1193
Db 273 GTAGTTGAATTCATAGTCCCGCAGTGCCTTTTCGCCAATACGCTCGCTCGATCAGCGT 214
QY 1194 CTCACGTATCTTTGTATGGAACGTCCTTTCACCTGAGCGGGAACAGTTATCCACTGTAA 1253
Db 213 CTCACGTATCTTTGTATGGAACGTCCTTTCACCTGAGCGGGAACAGTTATCCACTGTAA 154
QY 1254 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACGCTTGATATATTCGATGTC 1313
Db 153 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACGCTTGATATATTCGATGTC 94
QY 1314 ATCATAGATGATCAATTCATCGAGCAATCAATCAGTCAAAATATCTCGCCAAAGTAT 1373
Db 93 ATCATAGATGATCAATTCATCGAGCAATCAATCAGTCAAAATATCTCGCCAAAGTAT 34
QY 1374 GTAAATTTGATTGAACAATCCGACTTCTTCAA 1406
Db 33 GTAAATTTGATTGAACAATCCGACTTCTTCAA 1

RESULT 4
US-10-647-089-44/c
; Sequence 44, Application US/10647089
; Publication No. US20040063923A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE OF INVENTION: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/10/647,089
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-44

Query Match 49.3%; Score 693; DB 7; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAG 773
Db 693 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAG 634
QY 774 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTCGTCGAACAGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTACCCGGATGTAAGTTCGTCGAACAGCGCTCATCGACATACGAACG 514
QY 894 GGTGAGGGGCGCAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGTGAGGGGCGCAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGATTTGCCAGTCTGATATACC 1013
Db 453 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGATTTGCCAGTCTGATATACC 394

1014 GAGATAACTGCAATCGCATTCATATAGACGCTGTTGAGTGAAGAAAGATTCTGTGCTG 1073
Db
393 GAGATTAATCTGCAATCGCAATTCATATAGACGCTGTTGAGTGAAGAAAGATTCTGTGCTG 334
Qy
1074 TTCTTCGAGGTAATCGGCGGAGCGAGTCAGCGATCTCCGCAAAATGAGCGCGCGCT 1133
Db
333 TTCTTCGAGGTAATCGGCGGAGCGAGTCAGCGATCTCCGCAAAATGAGCGCGCGCT 274
Qy
1134 GTAGTTGAATTCAGTGCAGCGCGAGTCGCGTTCGCGCAATCGTGCCTCGATCAGCGT 1193
Db
273 GTAGTTGAATTCAGTGCAGCGCGAGTCGCGTTCGCGCAATCGTGCCTCGATCAGCGT 214
Qy
1194 CTCACGTATCTTTGATGGAAGAGTCCTTCACCTGAGCGGGAACAGTTATCCACTGTAA 1253
Db
213 CTCACGTATCTTTGATGGAAGAGTCCTTCACCTGAGCGGGAACAGTTATCCACTGTAA 154
Qy
1254 CCCCTGGCTCGTTTGGATCGAATTCCTGTTTCGCCAATCACGCTTGGTATATTTGCATGTC 1313
Db
153 CCCCTGGCTCGTTTGGATCGAATTCCTGTTTCGCCAATCACGCTTGGTATATTTGCATGTC 94
Qy
1314 ATCATAGATGATGAATTCATTCAGCAATGCAATCAGGTCAAAATATCTTCGCCAAGGTAT 1373
Db
93 ATCATAGATGATGAATTCATTCAGCAATGCAATCAGGTCAAAATATCTTCGCCAAGGTAT 34
Qy
1374 GTAAATTTGATTGAACAATCGGACTTCTTCAA 1406
Db
33 GTAAATTTGATTGAACAATCGGACTTCTTCAA 1

RESULT 5

US-09-894-844-43/c
; Sequence 43, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-43

Query Match 30.3%; Score 427; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTCTGTCGCGCA 60
Db 427 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTCTGTCGCGCA 368
Qy 61 TCTTTGATGATCGGAATTAAGATGTTCAGGCAATTTAAAGAGAAGCCACCGGACTCGCGG 120
Db 367 TCTTTGATGATCGGAATTAAGATGTTCAGGCAATTTAAAGAGAAGCCACCGGACTCGCGG 308
Qy 121 CATTCAGCATGTCAGCGTTCGCTTCGATGTAGCGGACCATTCGCTGTCACAGATTCA 180
Db 307 CATTCAGCATGTCAGCGTTCGCTTCGATGTAGCGGACCATTCGCTGTCACAGATTCA 248
Qy 181 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTTCGCGCTCCCGATCTATGCGCGCG 240
Db 307 CATTCAGCATGTCAGCGTTCGCTTCGATGTAGCGGACCATTCGCTGTCACAGATTCA 248
Qy 181 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTTCGCGCTCCCGATCTATGCGCGCG 240

247 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTTCGCGCTCCGATCTATGTCGCGCG 188
Qy 241 CCAGATGAAGTCTCGGTTTCGCGGACCTTCGAAACAGTAGTTCGCGCGCGGACCATTT 300
Db 187 CCAGATGAAGTCTCGGTTTCGCGGACCTTCGAAACAGTAGTTCGCGCGCGGACCATTT 128
Qy 301 CGGGGAGACGTCGATGCGGTTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 360
Db 127 CGGGGAGACGTCGATGCGGTTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 68
Qy 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTTCGAAATGGTCCGCGCATTTGACAA 420
Db 67 GTAGAGCCCCATAGCCACACGCTTAGATCGTTTCGAAATGGTCCGCGCATTTGACAA 8
Qy 421 TCGGCAC 427
Db 7 TCGGCAC 1

RESULT 6

US-10-388-902-43/c
; Sequence 43, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-43

Query Match 30.3%; Score 427; DB 7; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTCTGTCGCGCA 60
Db 427 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTCTGTCGCGCA 368
Qy 61 TCTTTGATGATCGGAATTAAGATGTTCAGGCAATTTAAAGAGAAGCCACCGGACTCGCGG 120
Db 367 TCTTTGATGATCGGAATTAAGATGTTCAGGCAATTTAAAGAGAAGCCACCGGACTCGCGG 308
Qy 121 CATTCAGCATGTCAGCGTTCGCTTCGATGTAGCGGACCATTCGCTGTCACAGATTCA 180
Db 307 CATTCAGCATGTCAGCGTTCGCTTCGATGTAGCGGACCATTCGCTGTCACAGATTCA 248
Qy 181 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTTCGCGCTCCCGATCTATGCGCGCG 240
Db 247 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTTCGCGCTCCCGATCTATGCGCGCG 188
Qy 241 CCAGATGAAGTCTCGGTTTCGCGGACCTTCGAAACAGTAGTTCGCGCGCGGACCATTT 300
Db 187 CCAGATGAAGTCTCGGTTTCGCGGACCTTCGAAACAGTAGTTCGCGCGCGGACCATTT 128
Qy 301 CGGGGAGACGTCGATGCGGTTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 360

Db 127 CGGGGAGAGCTGATGCCGGTGTAAATCAGTTTGAAGCCACGCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 420
Db 67 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 8
QY 421 TGGGCAC 427
Db 7 TGGGCAC 1

RESULT 7
US-10-647-089-43/c
; Sequence 43, Application US/10647089
; Publication No. US20040063923A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/647,089
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-43

Query Match 30.3%; Score 427; DB 7; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCGCTTGACAGATCAATAGGCGCATGGTGGTACAGATAGTACAGTCTGTCGCGCA 60
Db 427 ACCTGCGCTTGACAGATCAATAGGCGCATGGTGGTACAGATAGTACAGTCTGTCGCGCA 368
QY 61 TCTTTGATGATCGGAATAGATGTGAGGCAATTTAAAGAGAGCCACGCGACTCGCGG 120
Db 367 TCTTTGATGATCGGAATAGATGTGAGGCAATTTAAAGAGAGCCACGCGACTCGCGG 308
QY 121 CATTCAGCATGTGAGGCTGCTTCAGATGAGGCGCACCATTCGTTGTCACAGATTCA 180
Db 307 CATTCAGCATGTGAGGCTGCTTCAGATGAGGCGCACCATTCGTTGTCACAGATTCA 248
QY 181 GAGCAATTTGAATATTCACATCGGCGCATGATGTCGCTCCGCTCTATGCGCGCG 240
Db 247 GAGCAATTTGAATATTCACATCGGCGCATGATGTCGCTCCGCTCTATGCGCGCG 188
QY 241 CGCAGATGAGTCTGCGTTTCGCGCGCATTCGAAACGTTAGTGGCGCGCGCGCACCATTT 300
Db 187 CGCAGATGAGTCTGCGTTTCGCGCGCATTCGAAACGTTAGTGGCGCGCGCGCACCATTT 128
QY 301 CGGGGAGAGCTGATGCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGGTAGTCCA 360
Db 127 CGGGGAGAGCTGATGCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 420
Db 67 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 8
QY 421 TGGGCAC 427
Db 7 TGGGCAC 1

Db 7 TGGGCAC 1

RESULT 8
US-10-087-192-1528
; Sequence 1528, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1528
; LENGTH: 27204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1528

Query Match 2.8%; Score 39.8; DB 5; Length 27204;
Best Local Similarity 48.1%; Pred. No. 0.24;
Matches 113; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 411 GCATTGACAATGCGCACCAAGTGTGTCCTTCAAGCGCAAGCGCTTCCCGGCTTCGCCGTTCCAA 470
Db 19391 GCCTAGGGCTTGGCGAGCTGTGACCAAGGGGGCCACCTTGCCTGCTGAGCCCTGCCAG 19450
QY 471 TCGACGCGCGCGGTGCGGTGCTTTCGAGTTTCGATGCTAGTAACGCGGCCACGCTCAG 530
Db 19451 GTGACGCGCGAGCCAGAGCCCTGGCGTGGAGGTGAGTGCGGACGAGGGCTGGTGAG 19510
QY 531 CGAGCATGCTGCTTGGCTTTCGCCCATGAGCTGCTCAGATTTGTGTGTGGCGT 590
Db 19511 AGTGGCTGTTTCTCCCAACAGCTGACTTTGGGGTGTGAGGCGAGCTGACAGCGTCTGTGG 19570
QY 591 CGGTGGTGGTCCGAGACTATACCTTCAACAGTTTCATGCTGCGGAGCTGCGGCGG 645
Db 19571 CCAGAGGAGGTCTTTCATTTGGACTCCCTACTGTTGAGCTCGCTGCGGCGG 19625

RESULT 9
US-10-521-103-1
; Sequence 1, Application US/10521103
; Publication No. US20050136071A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Steven Gareth
; APPLICANT: Ritchie, Rachel Jane
; APPLICANT: Simard, Nathalie C.
; TITLE OF INVENTION: Hsp70 from Arthrobacter
; FILE REFERENCE: H-32534-A
; CURRENT APPLICATION NUMBER: US/10/521,103
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP03/07602
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: GB 0216414.3
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Arthrobacter
US-10-521-103-1

Query Match 2.7%; Score 38.4; DB 9; Length 2464;

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Best Local Similarity 48.6%; Pred. No. 0.22;
Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 205 CGACGCTATAGTCGGCTCCGATCTATCGCGCGCGCAGATGAAGTCTGCGTTGCGCC 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 515 CGACTGGACGCTCGGCATCGACACAAAGATACACCGCGCAGGAATCTCGCGCGCAC 574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 265 GACCTTCGAAAGTATGTCGGCGCGCGCACCAATTTCGGGGGAGAGCTGATCCGGTGT 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 575 CTGTATGAAGCTCAAGAACGACGCGCAGTCTTCTTGGCGGAAAGGTCACCGACGCGT 634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 325 AATCAGTTTGAAGCCACGCGATCTAGGTAGTCCAGTAGAGCCCATAGCCACAGCCCTA 384
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 635 GATCAGGTTCTGCTACTTCAAGACCGCGAGCGCGCAGGCCACCAAGAAGCCGGTGA 694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 385 GATCGTTGATGAAATGGGTCCGCGCATTGACAA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 695 GATCGCGCGCTGAACGTGCTGCGCATCGTCAACGA 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-10-338-110-119/c
; Sequence 119, Application US/10338110
; Publication No. US2004023254A1
; GENERAL INFORMATION:
; APPLICANT: Fuhrmann, Jeffrey J.
; APPLICANT: Romesser, James A.
; TITLE OF INVENTION: A Method To Assess Quorum Sensing Potential of Microbial
; FILE OF INVENTION: Communities
; CURRENT APPLICATION NUMBER: US/10/338,110
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (87)..(87)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (226)..(226)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (261)..(261)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (347)..(347)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (357)..(357)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (398)..(398)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (419)..(419)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (517)..(517)
; OTHER INFORMATION: n is a, c, g, or t
US-10-338-110-119

Query Match 2.7%; Score 37.8; DB 7; Length 536;
Best Local Similarity 10.0%; Pred. No. 0.16;
Matches 33; Conservative 170; Mismatches 128; Indels 0; Gaps 0;

QY 290 GCGCACCATTTTCGGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATC 349
    :||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 536 KCAEMRVYHBCBVMRMBKNVBCVVDYBGRDKSSVRRMGSMRVDBSKYBRBGSHKYG 477
    :||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 350 TAGGTAGTCCAGTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAAAATGGTCCGC 409
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
Db 476 HTVBYGRTCCRRSASGCSASSABYDKHYBVVYVYBDMWBSDKVRSCGRVCCRSBCGNTS 417
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 410 CGCATTGACAAATCGCACCGACGCTGTCAAAGCGCAACGCGCTCCCGCGCTTCGCGCTTCCA 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 SDVSHKBAVCCGWTSMKNHBGMWRSCBWCCTATSSVYVYVYVYVYVYVYVYVYVYVYVY 357
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 470 ATCGACGCGCGCGGTGCGGTGCTTCGCGCATGAAGCTGCCTCAGATTTGTGTGTGGCGG 529
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
Db 356 SBVMYBBGCNCCSVBWRSSHSGCKSWYTBSSASGVYKBHSSMSARAYMMBKAYSGCCMR 297
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
QY 530 GCGACATGGTGTGCGTTCGCGCTTCGCGCATGAAGCTGCCTCAGATTTGTGTGTGGCGG 589
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
Db 296 KTSGSDYGYGKGYGWAACGNGMADYTCCCANAYSKMBGATBSBKSOGYRKKBYB 237
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
QY 590 TCGGTGCGTGGTCCGAGACTATACCTCAA 620
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :
Db 236 YSBVGMVSRNRKVSRYRAABASNBMYTVA 206
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-156-761-1933/c
; Sequence 1933, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
```

US-10-437-963-48583
; Sequence 48583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(51221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 48583
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(485)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51244C.1
US-10-437-963-48583

Query Match 2.7%; Score 37.8; DB 6; Length 894;
Best Local Similarity 61.9%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 60; Conservative 0;
QY 403 GGTCCCGCGCATTCACATCGCGCCAGCTGGTCAAAAGCGCAACGCTGCGCGGCTTCGC 462
DB 192 GCGCCGACTCGCGGAGACAGCAGTTGGCCCGGCCACAGGCGCGCGGCTTCGT 133
QY 463 CGTCCAAATCGAGCGCGCGGTGCGGTGCTTCG 499
DB 132 CGTCGGCTTCGTGTCGCGCGGTGATCGGGTCTCG 96

RESULT 12
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 2.7%; Score 37.8; DB 6; Length 9025608;
Best Local Similarity 61.9%; Pred. No. 22; Mismatches 37; Indels 0; Gaps 0;
Matches 60; Conservative 0;
QY 403 GGTCCCGCGCATTCACATCGCGCCAGCTGGTCAAAAGCGCAACGCTGCGCGGCTTCGC 462
DB 2380428 GCGCCGACTCGCGGAGACAGCAGTTGGCCCGGCCACAGGCGCGCGGCTTCGT 2380487
QY 463 CGTCCAAATCGAGCGCGCGGTGCGGTGCTTCG 499
DB 2380488 CGTCGGCTTCGTGTCGCGCGGTGATCGGGTCTCG 2380524
RESULT 13

US-10-437-963-48583
; Sequence 48583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(51221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 48583
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(485)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51244C.1
US-10-437-963-48583

Query Match 2.6%; Score 36.6; DB 7; Length 485;
Best Local Similarity 43.8%; Pred. No. 0.41; Mismatches 156; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
QY 241 CGCAGATGAAGTCTGCTTGGCCCGACCTTTCGAAACGTAAGTGGCGCGCGCCGACCATTT 300
DB 85 CTCTCGAGTTGACAGCATCTGAAAGCTTCTCATGCAAGTGGATGCTTTACTTTATTA 144
QY 301 CGGGGAGAGCTCGATCGCGGTGTAATCAGTTTGAAGCCAGCGCATCTAGTAGTATCCA 360
DB 145 TTCATCAGTACAGTACATTTGTTGATCATATTTCTCTCAGTCTCTCAAAGGAATGAA 204
QY 361 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTTGACAA 420
DB 205 GGATACCCAGCAGCAGAGAACAAATTTATTCATCAGACATGCGATCAAGGAAGCAAC 264
QY 421 TGGGACACAGCTGGTCAAAAGCGCAACGCTTGGCGGCTTCCCGGTTCCCAATCGACCGCG 480
DB 265 TCATCACAATCTACACTAACTCCACGCTTACTCTTCTTCGTGAGAAACCTTCTCGGCT 324
QY 481 GCGGGTGGCTGCTTTCGAGTTTCGATCGTAGTAACGCGCCAGCTCAGCGAGCATGTT 540
DB 325 GAAACGCGGAGATCGAGCATCTTGGCATCGCGGTCGAGGATGAGCTCTGCGAGAGCGGC 384
QY 541 CGTTGCTCTTCGCGCATGAAGCTGCTCAGCATTTGTGTGTGGCGCTTCGCTGC 596
DB 385 ACCGTTGGCTGAGCATTTGAGGATCCCCCAGCAGCTGTGCGCGGCGGACATAGC 440

RESULT 14
US-10-156-761-2972/c
; Sequence 2972, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 01:43:06 ; Search time 459.429 Seconds
(without alignments)
6500.886 Million cell updates/sec

Title: US-09-673-476-1_COPY_1_1407

Perfect score: 1407

Sequence: 1 acctgcgttcgagatca.....caatcgcgactttcttcaac 1407

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 106136211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New.*

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1407	100.0	12732	8	US-10-802-796-1
2	693	49.3	693	12	US-11-143-401-44
3	427	30.3	498	12	US-11-143-401-43
4	36.2	2.6	88116	8	US-10-995-561-13351
5	36.2	2.6	222094	8	US-10-995-561-13244
6	35.4	2.5	622	6	US-09-925-065A-597843
7	34.6	2.5	388	6	US-09-925-065A-585977
8	34.6	2.5	496	6	US-09-925-065A-827710
9	34.2	2.4	634	6	US-09-925-065A-311017
10	33.8	2.4	810	6	US-10-467-657-5805
11	33.6	2.4	535	6	US-09-925-065A-288675
12	33.4	2.4	388	6	US-09-925-065A-585978
13	33.4	2.4	613	6	US-09-925-065A-411236
14	33.4	2.4	1194	6	US-09-925-065A-279367
15	33.2	2.4	600	8	US-10-750-185-707
16	33.2	2.4	600	8	US-10-750-623-707
17	33	2.3	388	6	US-09-925-065A-585976
18	33	2.3	634	6	US-09-925-065A-311018
19	33	2.3	634	6	US-09-925-065A-311019
20	32.6	2.3	164810	12	US-11-121-086-4

21	32.4	2.3	568	6	US-09-925-065A-649740	Sequence 649740,	
22	32.4	2.3	623	6	US-09-925-065A-839523	Sequence 839523,	
23	32.2	2.3	636	6	US-09-925-065A-328950	Sequence 328950,	
24	32	2.3	568	6	US-09-925-065A-649739	Sequence 649739,	
25	31.8	2.3	518	6	US-09-925-065A-737967	Sequence 737967,	
26	31.8	2.3	636	6	US-09-925-065A-328949	Sequence 328949,	
c	27	31.8	2.3	2157	8	US-10-467-657-761	Sequence 761, App
c	28	31.8	2.3	2319	8	US-10-858-730-148	Sequence 148, App
c	29	31.8	2.3	159695	12	US-11-121-086-56	Sequence 56, Appl
c	30	31.6	2.2	158692	12	US-11-121-086-30	Sequence 30, Appl
31	31.4	2.2	611	6	US-09-925-065A-482107	Sequence 482107,	
c	32	31.4	2.2	1020	8	US-10-467-657-7407	Sequence 7407, Ap
c	33	31.4	2.2	1020	8	US-10-467-657-8249	Sequence 8249, Ap
c	34	31.4	2.2	1085	8	US-10-883-512-131	Sequence 131, App
c	35	31.4	2.2	1398	8	US-10-750-185-24726	Sequence 24726, A
c	36	31.4	2.2	1398	8	US-10-750-623-24726	Sequence 24726, A
c	37	31.2	2.2	596	6	US-09-925-065A-813872	Sequence 813872,
c	38	31.2	2.2	165857	12	US-11-121-086-34	Sequence 34, Appl
c	39	31	2.2	629	6	US-09-925-065A-695006	Sequence 695006,
c	40	31	2.2	654	6	US-09-925-065A-630116	Sequence 630116,
c	41	31	2.2	1485	8	US-10-750-185-40943	Sequence 40943, A
c	42	31	2.2	1485	8	US-10-750-623-40943	Sequence 40943, A
c	43	30.8	2.2	317	12	US-11-043-752-2163	Sequence 2163, Ap
c	44	30.8	2.2	612	6	US-09-925-065A-790506	Sequence 790506,
c	45	30.8	2.2	94905	12	US-11-117-187-208	Sequence 208, App

ALIGNMENTS

RESULT 1

US-10-802-796-1
; Sequence 1, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: Patent In Ver. 2.2
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-1

Query Match	100.0%	Score 1407;	DB 8;	Length 12732;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1407;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACCTCGCTTCGAGAGATCAAAATAGCGGCATGGGTGACATAGTACAGGTGCTCGCGCA	60	
Db	1	ACCTCGCTTCGAGAGATCAAAATAGCGGCATGGGTGACATAGTACAGGTGCTCGCGCA	60	
QY	61	TCTTTGATCATCGGAATAGATGTGAGCAATTAAGAGAGCCAGCGGACTCGCG	120	
Db	61	TCTTTGATCATCGGAATAGATGTGAGCAATTAAGAGAGCCAGCGGACTCGCG	120	
QY	121	CATTGAGCATGCGAGCGTCTTCGATGTGAGCGCACCATTTCCGCTCCACGATTCA	180	

Db 121 CATTGAGCATGTCGAGGTCGCTTCGATGTCGAGCGACCATTCCTCGGTGTCACAGCATTTCA 180
QY 181 GACGAACATGTAATATTCACATCGCGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
Db 181 GACGAACATGTAATATTCACATCGCGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
QY 241 CGCAGATGAAGTCTGGGTTGCGCGGACCTTCGAAACGTAGTCGCGCGCGCGCGACCATTT 300
Db 241 CGCAGATGAAGTCTGGGTTGCGCGGACCTTCGAAACGTAGTCGCGCGCGCGCGACCATTT 300
QY 301 CGGGGAGACGTCGATGCGCGGTGTAATCAGTTTGAAGCGACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGACGTCGATGCGCGGTGTAATCAGTTTGAAGCGACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCATAGCCACAGCCCTAGATCGTTCGAAATAGGTCGCGCATTTGACAA 420
Db 361 GTAGAGCCCATAGCCACAGCCCTAGATCGTTCGAAATAGGTCGCGCATTTGACAA 420
QY 421 TCGGCACAGCTGCTCAAGACGGAACGCTGCGCGGCTTCGCGGTTCGAAATCGACGCGCG 480
Db 421 TCGGCACAGCTGCTCAAGACGGAACGCTGCGCGGCTTCGCGGTTCGAAATCGACGCGCG 480
QY 481 GCGGTGCGGTGCTTTCAGTTTCGATGCTAGTAAACGGGCCACGTCAGCGAGCATGCT 540
Db 481 GCGGTGCGGTGCTTTCAGTTTCGATGCTAGTAAACGGGCCACGTCAGCGAGCATGCT 540
QY 541 CGTTGCGTCTTCGCGCATGAAGTCTCAGATTTGCTGTGTGGCGCTCGGTGCGTGG 600
Db 541 CGTTGCGTCTTCGCGCATGAAGTCTCAGATTTGCTGTGTGGCGCTCGGTGCGTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTTCATGCGGAGCTCGCGGGGCAATGACCCAAAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTTCATGCGGAGCTCGCGGGGCAATGACCCAAAA 660
QY 661 CCGCGCGGACAGGTTCCGCGGACGAAGAGCGTGAGAGCATAGATAATTTCACTGGCGA 720
Db 661 CCGCGCGGACAGGTTCCGCGGACGAAGAGCGTGAGAGCATAGATAATTTCACTGGCGA 720
QY 721 CAGTACCTCAAAATAGTCGCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAAATCGAC 780
Db 721 CAGTACCTCAAAATAGTCGCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAAATCGAC 780
QY 781 AGCGGGGCTCGAAACCTCCGACAAATGCTTATATTCGCGGTAGCCGTCATATCGCAAC 840
Db 781 AGCGGGGCTCGAAACCTCCGACAAATGCTTATATTCGCGGTAGCCGTCATATCGCAAC 840
QY 841 CAAAGTTACCCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 900
Db 841 CAAAGTTACCCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 900
QY 901 GGGCCAGAGACATATTCGCTCGCTCGGCGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 901 GGGCCAGAGACATATTCGCTCGCTCGGCGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
QY 961 TTGCGGTGCGGTAAATTCGTAGTCCGACGAATTTGCCAGTCGCGTCTGTATACCGAGATAA 1020
Db 961 TTGCGGTGCGGTAAATTCGTAGTCCGACGAATTTGCCAGTCGCGTCTGTATACCGAGATAA 1020
QY 1021 CTGCAAAATCGCATTCGAATAGACGCTGTTGAGTAAGGAAGATTGCTGTGCTTCTTCG 1080
Db 1021 CTGCAAAATCGCATTCGAATAGACGCTGTTGAGTAAGGAAGATTGCTGTGCTTCTTCG 1080
QY 1081 AGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCGCTGTAGTTG 1140
Db 1081 AGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCGCTGTAGTTG 1140
QY 1141 AATTCTAGTCCGCGCAGTCGCTTTTCGCCCAATCGGTGCGTCTGATAGCGTCTCAAGT 1200
Db 1141 AATTCTAGTCCGCGCAGTCGCTTTTCGCCCAATCGGTGCGTCTGATAGCGTCTCAAGT 1200
QY 1201 ATCTTTTGATGAAACGTCCTTTCACCTCGACGGGAACAGTTATCCACTGTAAACCCCTCG 1260

Db 1201 ATCTTTTGATGAAACGTCCTTTCACCTCGACGGGAACAGTTATCCACTGTAAACCCCTGG 1260
QY 1261 CTCGTTTTCATCCGATTTCTGTTTGGCCAATCAGCGTTGGTATATTTGCATGTCATCATAG 1320
Db 1261 CTCGTTTTCATCCGATTTCTGTTTGGCCAATCAGCGTTGGTATATTTGCATGTCATCATAG 1320
QY 1321 ATGATGAATTCATCCAGCAATCAATCAGGTCAAAATATCTCTCGCAAGGTATGTAATTT 1380
Db 1321 ATGATGAATTCATCCAGCAATCAATCAGGTCAAAATATCTCTCGCAAGGTATGTAATTT 1380
QY 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407
Db 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407

RESULT 2

US-11-143-401-44/c
; Sequence 44, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-44

Query Match 49.3%; Score 693; DB 12; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.6e-211;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGCGACAGTACCTCAAAATAGTCGCGAGCCTCGGCTCCGACGTTTAAAGACGATCCAG 773
Db 693 CTGGCGACAGTACCTCAAAATAGTCGCGAGCCTCGGCTCCGACGTTTAAAGACGATCCAG 634
QY 774 AATCGACACGCGGGCTCGAACCTCCCACAATTTGCTTATATTAATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGCGGGCTCGAACCTCCCACAATTTGCTTATATTAATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTTACCCGGATGCTAAGTTTCGCAACACGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTTACCCGGATGCTAAGTTTCGCAACACGCGCTCATCGACATACGAACG 514
QY 894 GGCTGAGGGCCAGAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGCTGAGGGCCAGAGACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTGGCGTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCGCGTGTGATACC 1013
Db 453 CTCGGTCTTGGCGTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCGCGTGTGATACC 394
QY 1014 GAGATAACTGCAAAATCGCAATTCGAATAGACGCGCTGTTGAGTAAGGAAGAAATTCGTGTGCTG 1073
Db 393 GAGATAACTGCAAAATCGCAATTCGAATAGACGCGCTGTTGAGTAAGGAAGAAATTCGTGTGCTG 334

QY 1074 TTCTTCAGGTAAATCGCGCGAGCCAGTCAAGGATCTCCGCAAAATGAGCGCGCGCT 1133
Db 333 TTCTTCAGGTAAATCGCGCGAGCCAGTCAAGGATCTCCGCAAAATGAGCGCGCGCT 274
QY 1134 GTAGTTGAATTCAGTCCCGCAGTGCCTTTCCGCCAATCGGTCCGTCGATCAGCGT 1193
Db 273 GTAGTTGAATTCAGTCCCGCAGTGCCTTTCCGCCAATCGGTCCGTCGATCAGCGT 214
QY 1194 CTCACGTATCTTTTGATGAGAAACGTCTCCCTTCACTGACCGGGAACAGTTATCCACTGTAA 1253
Db 213 CTCACGTATCTTTTGATGAGAAACGTCTCCCTTCACTGACCGGGAACAGTTATCCACTGTAA 154
QY 1254 CCCTGCTCGTTTGATGAGAAACGTCTCCCTTCACTGACCGGGAACAGTTATCCACTGTAA 1313
Db 153 CCCTGCTCGTTTGATGAGAAACGTCTCCCTTCACTGACCGGGAACAGTTATCCACTGTAA 94
QY 1314 ATCATAGATGATGAATTCATGAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1373
Db 93 ATCATAGATGATGAATTCATGAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 34
QY 1374 GTAATTGATTGAACAAATCGCGACTTCTTCTCAA 1406
Db 33 GTAATTGATTGAACAAATCGCGACTTCTTCTCAA 1
RESULT 3
US-11-143-401-43/c
; Sequence 43, Application US/11143401
; Publication No. US2006002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-43
Query Match 30.3%; Score 427; DB 12; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.3e-126; Mismatches 0; Indels 0; Gaps 0;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCTGCGCTTGACAGATCAATAGGCGCATGGGTGAGCATAGTACAGGTGCTCGCGCA 60
Db 427 ACCTGCGCTTGACAGATCAATAGGCGCATGGGTGAGCATAGTACAGGTGCTCGCGCA 368
QY 61 TCTTTGATGATCGGAAATAGATGTCAGGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 367 TCTTTGATGATCGGAAATAGATGTCAGGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
QY 121 CATTGACATGTCAGCGTCGCTTCCATGTGAGCGCACCATTCGCGTCCCAAGATTCA 180
Db 307 CATTGACATGTCAGCGTCGCTTCCATGTGAGCGCACCATTCGCGTCCCAAGATTCA 248
QY 181 GACGAAATTGAATATTTCCACTCGCGACGCTATAGTCCGCTCCGATCTATGCGCGCG 240

Db 247 GACGAACATTGAATATTTCCACTCGCGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 188
QY 241 CGCAGATGAAGTCTGCGTTTCGCCCGGACCTTCGAAACCTAGTCCGCGCGCGCGACCAATTT 300
Db 187 CGCAGATGAAGTCTGCGTTTCGCCCGGACCTTCGAAACCTAGTCCGCGCGCGCGACCAATTT 128
QY 301 CGCGGAGAGCGTGCATGCCGCTGTAATCAGTTTGAAGCCACCGCATCTAGGTAGTCCA 360
Db 127 CGCGGAGAGCGTGCATGCCGCTGTAATCAGTTTGAAGCCACCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCCATAGCCACAGCTAGATCGTTGATCGAAATGCGTCCGCGCATTTGACAA 420
Db 67 GTAGAGCCCCATAGCCACAGCTAGATCGTTGATCGAAATGCGTCCGCGCATTTGACAA 8
QY 421 TCGCGAC 427
Db 7 TCGCGAC 1
RESULT 4
US-10-995-561-13351
; Sequence 13351, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13351
; LENGTH: 88116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13351
Query Match 2.6%; Score 36.2; DB 8; Length 88116;
Best Local Similarity 62.9%; Pred. No. 3; Mismatches 33; Indels 0; Gaps 0;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 403 GGTCCGCGCGCATTTGACAAATGCGCACGAGCTGGTCAAGAGCAACGCTGCCCGCTTCGC 462
Db 5737 GTTCTGACGATCTCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5796
QY 463 CGTTCCAAATCGACGCGCGCGCGCGCGCGTGCCT 491
Db 5797 CTCTCAAAACCCCTCCGCGCGCGCGCGCGCGCTT 5825
RESULT 5
US-10-995-561-13244/c
; Sequence 13244, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13244
; LENGTH: 222094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13244
Query Match 2.6%; Score 36.2; DB 8; Length 222094;

```
Best Local Similarity 62.9%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 403 GGTCCGCCGCAATGACAATCGCACAGCTGTGTCAAAGCGCAACGCTGCGCGCTTCGC 462
Db 213061 GTTCTGCAGCATCTCCAATGCCCGCAGCCGCGCAGCCGCGCGCGCGCGCGCGC 213002

QY 463 CGTTCCAATCGACGCGCGCGGGTGCCT 491
Db 213001 CTCTCAAAACCCCTCCGCGCAGGAGCCTT 212973
```

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RESULT 6
US-09-925-065A-597843/c
; Sequence 597843, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597843
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-597843
```

```
Query Match 2.5%; Score 35.4; DB 6; Length 622;
Best Local Similarity 49.7%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1202 TCTTTTGATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGTAAACCCCTGGC 1261
Db 619 TCTGGGCTACAGCAGTCTCCACCTAGCCTCTGAGGTGTGCACTATGATGCTGAC 560

QY 1262 TCGTTTGTGATCCGATTTCTGTTTGGCAATCAGCTTGGTATATTGCATGTCATCATAGA 1321
Db 559 TAATGATTAATTTTTTTTTTTTTTTTGTAGAAACAGATTCTCTCAATGTTGCCCGAGCTGA 500

QY 1322 TGATGAATTCATCGACGAATGCAATCAGTCAAAATATCTCGCCAAAGTATGTAATTGG 1381
Db 499 TTTCAAAATCTTGGGCTCAAGCAATCTCCACCTTAGCTCTCCAAAGTGTGGGATTAG 440

QY 1382 A 1382
Db 439 A 439
```

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RESULT 7
US-09-925-065A-585977
; Sequence 585977, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 585977
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-585977
```

```
Query Match 2.5%; Score 34.6; DB 6; Length 388;
Best Local Similarity 49.2%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 88; Conservative 1; Mismatches 90; Indels 0; Gaps 0;

QY 1075 TCTTCAGGTAAATCGCGCGCAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTG 1134
Db 143 TCGCCGTGTCTCATGCGAGGGACCCAGTCGAGAGTGATTGAATCATGGGGGTGGTTTC 202

QY 1135 TAGTTGAATTTAGTCCCGCCAGTCGCTTTTCGCCCAATCGGTGCGGTCGATCAGCGTC 1194
Db 203 TCGTCTGTTCTCATGATAGYGAGTGAGTTCTCATGAGATCTGATGATTTTATAAGCTAC 262

QY 1195 TCAGGTATCTTTTGATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGAA 1253
Db 263 TGGCAATTTCCCTGCTGCACCTTATTCTCTCCCTTTCTTTATAAATTACCCAGTCTGA 321
```

```
RESULT 8
US-09-925-065A-827710
; Sequence 827710, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827710
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827710
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```
Query Match 2.5%; Score 34.6; DB 6; Length 496;
Best Local Similarity 53.3%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1209 ATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGTAAACCCCTGGCTCGTTT 1268
Db 89 ATAAGAAGGTAACTTCTGCTGGAAGAGTACCAGTCTCTTTTCTGTTGATGATGAT 148

QY 1269 GATCCGATTTCTGTTTCGCCAATCAGCTTGGTATATTGTCATCATAGATGATGA 1328
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Db 149 GTTAAATGTTACTTTTATCTCCACCATAGATATGGTATTAACAAAGGGTTGGTAA 208
QY 1329 TTCATCGACGAATGCAA 1345
Db 209 TTCATTGACAGAACAA 225

RESULT 9

US-09-925-065A-311017/c
; Sequence 311017, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311017
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-311017

Query Match 2.4%; Score 34.2; DB 6; Length 634;
Best Local Similarity 52.6%; Pred. No. 1.8;
Matches 72; Conservative 1; Mismatches 64; Indels 0; Gaps 0;
QY 1209 ATGGAACGTCCTCCACCTGGACGGGAACAGTTATCCACTGTAAACCCCTGGCTCGTTTT 1268
Db 163 ATAAGAAGGTAACTTCGTCTGGAAGGAAGTACCATGCTCTTTTCTGTGTCATGTTAT 104
QY 1269 ATCCGATTTCTGTTTCGCAATCAGCTTGGTATATTCATGTCATCATAGATGAA 1328
Db 103 GTTAAATGTTACTTTTATCTCCACCATAGATATGGTATTAACAAAGGGTTGGTAA 44
QY 1329 TTCATCGACGAATGCAA 1345
Db 43 TTCATTGACAGAACAA 27

RESULT 10

US-10-467-657-5805
; Sequence 5805, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5805

; LENGTH: 810
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5805

Query Match 2.4%; Score 33.8; DB 8; Length 810;
Best Local Similarity 51.7%; Pred. No. 2.7;
Matches 77; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 191 GAATATTCACCTCGGACCGCTATAGTCCCGCTCCCGATCTATGCGCGCGGAGATGAA 250
Db 21 GAATTTTCCGTCGGTTCGCTGATTTTCCGCGCGAGGTTGAGGAAGCCGTTTCATCGCGT 80
QY 251 GTCTGCTTCCGCGCGACCTTCGAAACGTAGTGGCGCGCGCACCACCATTTTCGGGGGAGAC 310
Db 81 GTATGCGTTTGACGACGCGCGGACGATATGCGGACGAGGCGAGTATGCCGTTCTGAAGC 140
QY 311 GTCGATGCGCGGTGTAATCAGTTTGAAGC 339
Db 141 CAGGTTGTCGGGTTGGAGGGTTTTCGCGC 169

RESULT 11

US-09-925-065A-268675
; Sequence 268675, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268675
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-268675

Query Match 2.4%; Score 33.6; DB 6; Length 535;
Best Local Similarity 57.7%; Pred. No. 2.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1291 TCACGCTTGGTATATTCGATGTCATCATAGATGAATTCATCGACGAATCAATCAGG 1350
Db 350 TCATTTCTGTTATATCTCAACTAAATCAGAGTTGAGGAACCCAGGGGAAATGCACCTCAGG 409
QY 1351 TCAAAATATCTTCGCGCAAGGTATGTAATTTGATTGAACAAATCGC 1394
Db 410 GCATATCATATTTGCTCCAGAGATGTAATTTCTCTGCAAACTGCG 453

RESULT 12

US-09-925-065A-585978
; Sequence 585978, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135


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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT09508
US-10-750-185-707

Query Match      2.4%; Score 33.2; DB 8; Length 600;
Best Local Similarity 61.6%; Pred. No. 3.7;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1298 TGGTATATTGCATGTCATCATAGATGATGAATTCATCGACGCAATGCAATCAGGTCAAAT 1357
Db 139 TGGAAATCTGCATGTAGTATTAAAAAACATTATCTTGAACATATGGCATCAGGAAAAAT 198

QY 1358 ATCCTCGCCAAGGTATGTAATTTGAT 1383
Db 199 ATACCCCTGGAAGATGTGAATTTAAT 224

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Job time : 461.429 secs

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